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Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

Result No.

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Sequence 1,
Sequence 2,
Sequence 2,
Sequence 2,
Sequence 2,
Sequence 10,
Sequence 10,
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08729103
; Sequence 1, Application US/08729103
; Patent No. 5837841
; GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                 US-07-893-929A-5
PCT-US92-10344-5
US-07-893-929A-2
PCT-US92-10344-3
US-07-893-929A-3
US-07-893-929A-1
US-07-US92-10344-1
PCT-US92-10344-1
PCT-US92-10344-1
PCT-US92-10344-1
US-08-109-652-2
US-08-09-725-6
US-09-10344-10
PCT-US92-10344-10
US-09-113-788-4
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DGS
SOFTWARE: FASTESO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER: FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REJEMBNISTATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
STRANDENESS: single
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
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US-08-729-103-1
204
1198.5
1198.5
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1189
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    Sequence 2, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                           December 31, 2003, 09:11:17; Search time 41 Seconds (without alignments) 163.052 Million cell updates/sec
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878
1 MASRSMRLLLLLSCLAKTGV......LTWSSNECNKRQHFLCKYRP 158
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                     version 5.1.6
- 2003 Compugen Ltd.
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US-08-468-413-2
US-08-468-413-2
US-08-7169-2
US-08-70169-2
US-08-709-103-3
US-08-709-662-7
US-08-709-662-5
US-08-709-662-5
US-08-709-662-5
US-08-709-662-5
US-08-709-662-5
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US-08-709-662-3
US-07-893-929A-7
PCT-US92-10344-7
US-08-822-261-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                     GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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Gaps

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PCT-US95-07169-2
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                                                                                                  61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                     61 YGNGAHLASILISLKBASTIABYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOS
                             1 MASRSWRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08468413
Patent No. 5861494
GENERAL INFORMATION:
APPLICANT: LI, FT AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCETATION STATEMENT S. SCETABLE MORD PERFECT S. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,413
FILING DATE: 06 JUN 95
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
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STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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Best Local Similarity 100.0%; Pred. No. 2e-88;
Matches 158; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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Sequence 2, Application US/09162508
| Patent NO. 6080722
| GENERAL INFORMATION:
| APPLICANT: LI, ET AL.
| TITLE OF INVENITON: Human Colon Specific Gene
| NUMBER OF SEQUENCES: 6
| CORRESONDENCE ADDRESS:
| ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
| ADDRESSEE: CECCHI, STEWART & OLSTEIN
| STREET: 6 BECKER FARM ROAD
| CITY: ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9507169
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,508
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,413
FILING DATE: 06 JUN 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRARION NUMBER: 36,134
                                                                                                                                                                                                                                                                                                                                            ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEBHONE: 201-994-170
TELEFAX: 201-994-174
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                 STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: LINEAR
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52 SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .5e-20;
es 51; Indels
    Patentin Release #1.0, Version #1.25
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Sequence 3, Application US/08729103
Fatent No. 5837841
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Golf, Surya K.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.0%; Score 254.5; 30.6%; Pred. No. 3.5
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOCTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REPERNCE/DOCKET NUMBER: 0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: 1:-
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FABLERO '''
INDERNO.
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.6%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-401-530A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MASRSWRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 878; DB 5; Length 158;
Best Local Similarity 100.0%; Pred. No. 2e-88;
Matches 158; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07169
FILING DATE: 06 JUN 95
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08401530A
Patent No. 5834590
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSES: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                NAME: FERRARO, GREGORY D. REGISTRATION NUMBER: 36,13* REFERENCE/DOCKET NUMBER: 37 FELECOMMUNICATION INFORMATION TELECHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAID:
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i: 158 AMINO ACIDS
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-1895-07169-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
ROSELAND
NEW JERSEY
                                        USA
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Gaps

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52 SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 RISCPEGTINAYRSYCYYFNEDPETWVDADLYCQNMNSG-NLVSVLTQAEGAFVASLIKES 91
                                                                                                                 --CAPGWFYHKSNCYGYFRKLRNW
                                                                                                                                                      5 KYFILLSCL------MVLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGY
                                                                                                                                                                                                                                                                              110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKROHFLCKYR 157
                                                                                                                                                                                                                                                                                                    29;
                                   Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 166;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: BANDMAN, Olga
APPLICANT: GO11, SULTA K.
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
CITYS: Palo Alto
STATE: CA
COUNTRY: US
                                Query Match 29.0%; Score 254.5; DB 2 Best Local Similarity 30.6%; Pred. No. 3.5e-20; Matches 52; Conservative 38; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 240; DB 2; 34.3%; Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                 7 RLLLLSCLAKTGVLGDIIMRPS-
                                                                                                                                                                                                                                                                                                                                                                                                 US-08-729-103-4; Sequence 4, Application US/08729103; Patent No. 5837841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAK: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: li
US-08-709-662-7
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                                                                                                                                                                                                                                                                                                                                                                                                                        S KYPILLSCL------MVLSPSQQEABEDLPSARITCPEGSNAYSSYCYYFMEDHLSW
                                                                                                                                                                                                                                                                                                                     --CAPGWFYHKSNCYGYFRKLRNW
                                                                                                                                                                                                                                                                              Indels 29; Gaps
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                                                                                                                                                                                                                                      DB 2; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rogenberg, Lawrence
APPLICANT: Noguid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEGENESIS
TOWNER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
THANG DATE: 435
                                                                                                                                                                                                                                                         3.5e-20
                                                                                                                                                                                                                                    Query Match
29.0%; Score 254.5;
Best Local Similarity 30.6%; Pred. No. 3.5e
Matches 52; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Kagen, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 RLLLLLSCLAKTGVLGDIIMRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08709662
Patent No. 5840531
GENERAL INFORMATION:
              SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rattus rattus
                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                      LIBRARY: GenBank
CLONE: 393209
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                          92 STDDSNVWIGLHDPKKNRRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGFKKWKD 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| || :| || |:| || || || || 65 DLACQKRPSG-HLVSVLSGSEASFVSSLIKSSGNSGONVWIGLHDPTLGGSPNRGGWEWS 123
87 QRSQP-IWIGLHDPQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VALITMSWMLLSSLMLLSQVQGEDAKEDVPTSRISCPKGSRAYGSYCYALFSVSKSWFDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Score 231; DB 2; Length 174; 32.4%; Pred. No. 1.4e-17; Live 28; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                              APPLICANT: Vinik, Aaron I.

APPLICANT: Pitcanger, Gary L.

APPLICANT: Refaeloff, Ronit

APPLICANT: Rosenberg, Lawrence

APPLICANT: Duguid, William P.

TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC

TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILLING DATE: 22-FEB-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEB: Banner & Allegretti
                                                                                                                                                                                                                           Sequence 5, Application US/08401530A
Patent No. 5834590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1001 G Street, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEC ID NO: 5
                                                                               144 NECNKRQHFLCKYR 157
                                                                                                          | |: |:||::
152 ESCEKKFSFVCKFK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 174 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 55; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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RESULT

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55 ELECQSYGNGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDPQKRQQ-----WQWI 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Vinik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Depuid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pitterger, Gary L.
Rafaeloff, Ronit
Rosenberg, Lawrence
Duguid, William P.
VENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 231; DB 2;
Pred. No. 1.4e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/709,662
09-SEP-1996
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Patent No. 5834590

GENERAL INFORMATION:

APPLICANT: Vinik, Aaron I.

APPLICANT: Rafaeloff, Ronit

APPLICANT: Rafaeloff, Ronit

APPLICANT: Rosenberg, Lawrence
                                                                                                                                                                                                                                                        Banner & Witcoff, Ltd.
Application US/08709662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REPERENCE/DOCKET NUMBER: 005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                          Hashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%;
32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.44
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                             ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 09-SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                       STATE: D.C
                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-401-530A-6
                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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us-09-525-041-2.rai

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Floppy disk
                                                                                                                                                                                                                                                                        TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Rattus rattus US-08-709-662-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5514582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5514582-15
;Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 VNNNQDIWIHLHDPTWGQQPNGGGWEWSNSDVLNYLNWDGDPSSTVNRGNCGSLTATSEF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Vinlk, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Refaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Rosenberg, Lawrence
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES:
CORRESSEDENCE ADDRESS:
ADDRESSEE: Banner:
STRPPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 174;
                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.0%; Score 228.5;
illarity 34.5%; Pred. No. 2.6e
Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TITLE OF INVENTION: ISLET NEGGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
                                                          SEE: Banner & Allegretti
P: 1001 G Street, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08709662
Patent No. S840531
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 LTWSSNECNKROHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 LKWGDHHCDVELPFVCKFK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1001 G Street, N.W CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                       ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 48; Conserv
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TOPOLOGY:
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86 YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CYYFMEDHLSWAEADLFCQNMNSG-YLVSVLSWAEGNFLASLIKESGTTAAN-VWIGLHD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 CYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID ITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID IMMUNOSICABLINS: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
APPLICATION NUMBER: 986,931
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.0%; Score 228.5; DB 2; Best Local Similarity 34.5%; Pred. No. 2.6e-17; Matches 48; Conservative 25; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.4%; Score 223; DB 6; 34.7%; Pred. No. 6.1e-17; tive 30; Mismatches 41
                                                                                 FILING DATE: 09-SEP-1996
CLASSIFICATION: 435-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : |: |:||::
155 LKWGDHHCDVELPFVCKFK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 LTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                               32,141
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
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APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,1
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                                                                                                                                                                                            APPLICANT: Divanna, Juan-Lucio
APPLICANT: Dayorn, Jean-Charles
APPLICANT: Bagorn, Jean-Charles
APPLICANT: Keim, Volker
APPLICANT: Keim, Volker
APPLICANT: Sarles, Jacques
APPLICANT: Sarles, Jacques
TITLE OF INVENTION: Detection of Pancreatitis-Associated
TITLE OF INVENTION: Disease (as amended).
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STRET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 NGAHLASILSLKEASTIAEYISGYQRSQP-IWIGLHDPQKRQQ-----WQWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LLLSCL-AKTGVLGDIIMR--PS----CAPGWFYHKSNCYGYFRKLRNWSDAELECOSYG 62
99 PQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLFWSSNECNKRQHFLC 154
                         60 PKNNRRWHWSSGSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKRWRDNSCDAQLSFVC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AWERNPSTISSPGHCASLSRSTAFLRWKDYNCNVRLPYVCKF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 SW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             • ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,637
FILING DATE: 30-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.2%; Score 221; 32.7%; Pred. No. 1
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Sequence 4, Application US/08401530A

Patent No. 5834590

GRNERAL INFORMATION:

APPLICANT: Vinik, Aaron I.

APPLICANT: Pittenger, Gary L.
                                                                                                                                    Sequence 2, Application US/08464637
Patent No. S834214
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 175 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-464-637-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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63 NGAHLASILSLKEASTIAEYISGYQRSQP-IWIGLHDPQKRQQ-----WQWIDGAMYLYR 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.2%; Score 221; DB 2; Length 175;
Best Local Similarity 32.7%; Pred. No. 1.7e-16;
Matches 53; Conservative 29; Mismatches 64; Indels 16; Gaps
                                                 APPLICANT: Rosenberg, Lawrence
APPLICANT: Diguid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 SW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKY 156
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|| : || : || : || : || : || : || : || : || : || : || :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FRE1195
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan: Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.48743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 31, 2003, 09:16:48
Job time : 43 secs
                                                                                                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 175 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
Rafaeloff, Ronit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-401-530A-4
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us-09-525-041-2.rst

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:

December 31, 2003, 09:22:09; Search time 2056 Seconds (without alignments) 1867.756 Million cell updates/sec

US-09-525-041-2 ritle:

878
1 MASRSMRLLLLLSCLAKTGV.....LIWSSNECNKRQHFLCKYRP 158 Perfect score: Sequence:

BLOSUM62 Scoring table:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

22781392 seqs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: * Database :

em_esthum:*
em_estin:*
em_estin:*
em_estin:*
em_estil:*
em_estil:*
em_htc:*
gb_esti:*
gb_esti:*
gb_esti:*
gb_esti:*
gb_esti:*
gb_esti:* em_estba:*

gb_est5:*
em_estfun:*
em_estom:*

em_gas_hum:* em_gss_inv: em_gss_pln: em_gss_vrt: 113 ... 119 ... 119 ... 119 ... 119 ... 129 ...

em_gss_fun:* em_gss_mam:* em_gss_mus:* em_gss_pro:

em gss rod: *
em gss phg: *
em gss vrl: *
gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

cription	764955 K-EST004	72617 K-EST005	70898 60271910	4658 K-EST004	SYLOR K-ESIOUS	34067 K-EST	72152 60144625	57953 EST37002	3845 60236654	38204 K-EST006	1779 EST186601	56113 602367	1222 nd38e09	0123910	19915 K-ESTO05	2851 K-ESTO	21464 K-EST009	3533 EST179353	5990 EST1877	1573 EST1864	3019 EST1788	789 EST1788	862 EST187607	SELVY K-ESTO	15/ ESTIB//	9 EST1854	9144 K-ESTO	348 EST188510	2702 K-ESTO	200 EST185134	796494 K-ESTO	33214 CM3-CFU3	100004601	16249 EST18802	X708034 BY7	8049 Mus mu	38108 ug48f05	08438 Mue musc	M790284 K-EST007	13643 RZPD Mus	9 BY7083
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ALIGNMENTS

BM764955 663 bp mRNA linear EST 04-MAR-2002 K-EST0046563 S3SNU1681 Homo sapiens cDNA clone S3SNU1681-12-E07 5', BM764955.1 GI:19094570 mRNA sequence. BM76495 RESULT 1 BM764955 LOCUS DEFINITION

EST. ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 663)

REFERENCE

AUTHORS

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207 CTGGGTGATATCATCATGAGACCCAGCTGTGTCTCTGGATGGTTTTACCACAAGTCCAAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM772617.1 GI:19102232
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Homo sapiens
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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BM772617
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             Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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                                                                                                                                                                                                                    Contact: Kim YS

Genome Research Center

Genome Research Institute of Bioscience & Biotechnology

Korea Research Institute of Bioscience & Biotechnology

Korea Research Institute of Bioscience & Biotechnology

Kare Besearch Institute of Bioscience & Biotechnology

Tel: +82-42-860-4409

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 12 row: E column: 07

High quality sequence stop: 663.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue_type="Ascites"

cell_type="Lymphoblast-like"

cell_line="SNU-16"

lab_host="Top10p""

clone_lib="S3SNU16s1"
                                                                                                                                         21C Frontier Korean EST Project 2001
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="S3SNU1681-12-E07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ltype="mRNA"
xref="taxon:9606"
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Best Local Similarity:
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DB:
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JOURNAL
COMMENT
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LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40

ò 셤 ò

ORIGIN

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/clone libe 535NU1681"
/note= Torgan: Stomach; Vector: pT218RP1; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA linkase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM772617 708 bp mRNA linear EST 04-MAR-2002
K-EST0056822 S3SNU1681 Homo sapiens cDNA clone S3SNU1681-14-G04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 708) to 708, Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R., Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                       140
                                                                                                                                                               101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
267 recrarestractricassaactisassaactisatetatisessagetesagetesaget 326
                                                        80
                                                   121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                    141 TrpSerSerAanGlucysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
Contact: Kim YS
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Exeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4409
Pax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: yongsung@mail.kribb.re.kr
Plate: 14 row: G column: 04
High quality sequence scop: 708.
Location/Qualifiers
1. 708
/organism="Homo sapiens"
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/clone="S3SNU1661-14-G04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim, Y.S.
21C Frontier Korean BST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="Ascites"
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTP/DTP

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCML669 row: k column: 02

High quality sequence stop: 731.
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 822)
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priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coil DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5, primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinhaled single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG770898 822 bp mRNA linear EST 15-MAY-2001 602719106F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4839673 5',
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1 (bases 1 to 665)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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388 GAGTACATAAGTGGCTATCAGAGAAGCCAGCGGATATGGATTGGCCTGCACGACCCACAG 447
                          101 LyshrgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
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                                                                                                                                  141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S3SNU1681-7-G11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: yongsung@mail.kribb.re.kr
Plate: 7 row: G column: 11
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Location/Qualiflers
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Contact: Kim YS
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K-EST0008559 S3SNU16 Homo sapiens cDNA clone S3SNU16-3-G07 5', mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mismatches:
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567

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(1990), Cancer Res 50: 2773-2780."
                                                                                                                                                                                                                    BM852931 600 bp mRNA linear EST 06-MAR-2002
K-EST0134255 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-130-C07
S', mRNA sequence.
BM852931
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 600)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Xim,Y.S.

21C Prontier Korean EST Project 2001

Unpublished
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 600)
      121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr
                                   508 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT
                                                                                      Contact: Kim YS
Genome Research Center
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S2 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 130 row: C column: 07
High quality sequence stop: 600.
Location/Qualifiers
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EST.
Homo sapiens (human)
Homo sapiens
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Pred. No.:
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BM852931
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                                                                                                                                                                                                                                                                                                                                                                                                                    / Otone __IDB=`SASNULD.
// Otole__TOB=`SASNULD.
// Otole__Tobaon: Stomach; Vector: pT218RPl; Site__I: ECORI;
Site__2: NotI; The poly (A) + RNA was dephosphorylated with
Dacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including ECOR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The GT-tailed vector was
adjusted to have about 60nt. The GDNA vector was
circularized with E. coli DNA ligase after digestion of
ECORI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
competent cells E. coli Toplof* by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 TACGGAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 GluTyr1leSerGlyTyrGlnArgSerGlnProlleTrp1leGlyLeuHigAspProGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla 80
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Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470

Email: 92-42-860-4409

Email: yongsung@mail.kribb.re.kr
Plate: 3 row: G column: 07

High quality sequence stop: 628.
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601/11/2 BST 20-OCT-2000 60146259F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850358 5', BE872152
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11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ATGGCTTCCAGAAGCATGCGCTCCTATTGCTGAGCTGCCTGGCCAAAAACAGGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCc
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
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Homo sapiens
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K-EST0136364 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-145-C05
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/clone_lib="S128NU16"
/clone_l
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R. Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                     CTGGGTGATATCATCATGAGACCCAGCTGTGCTCTGGATGGTTTTACCACAAGTCCAAT
                                                                                                                                             GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGGTATGGATTGGCCTGCACACAC
                                                                                                          CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                             61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 AAGTCCATGGGTGGGAACAAGGCTCTGTGCTGGATGAGCTCCAATAACAACTTTTTAACT
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLys 155
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Plate: 145 row: C column: 05
High quality sequence stop: 667.
Location/Qualifiers
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BG253845 908 bp mRNA linear EST 13-FEB-2001 602366542F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4474691 5', mRNA sequence.
BG253845
BG253845.1 GI:12763661
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: john@digr.org
        Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J.
                                                                                                                                                                                                                      1. .664
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5 a 160 c 173 g 156 t
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        ,I.E., Saeed,/
Quackenbush,J
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/mol_type="mRNA"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
# Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
# Colone insert size 1.8 kb. Library constructed by Life
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 664)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
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Query Match:
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RESULT 9
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REFERENCE AUTHORS

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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 AAGAGGCAGCAGTGGCAGTGGATTGATGGGGCCCATGTATCTGTACAGATCCTGGTCTGGC 495
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                            Eukaryorta.

Mammalia: Butheria: Primates; Catarrhini; Hominidae; Homo.

I (bases I to 908)

NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                          con Library Preparation: Life Technologies, Inc.
con Library Preparation: Life Technologies, Inc.
con Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10299 row: c column: 12
High quality sequence stop: 734.
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                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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96.20%
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Homo sapiens (human)
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                  Homo sapiens
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/clone libe Sisbauls"
//clone libe Sisbauls"
//clone libe Sisbauls"
//clone libe Sisbauls Stomach, Vector: pTZ18RP1; Site 1: ECORI;
Site 2: Not1: The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
CDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The CDNA vector was
circularized with E. coli DNA ligase after digestion of
ECORI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli ToplOF' by electroporation method.
The CDNA libraries constructed by this method are
full-length enriched cDNA library."
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Kin, Y.S.
21C Frontier Korean EST Project 2001
Upublished
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Sz Boeun-dong Yuseong-gü, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 34 row: B column: 05
High quality sequence stop: 580.
Location/Qualifiers
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BG256113 968 bp mRNA linear EST 13-FEB-2001 602367238F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE.4475648 5',
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                       Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                       1. .551
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Homo gapiens (human)
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  Fax: 3018699423
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I (basea 1 to 531)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A., Bult

C.J., Lee, N.H., Kirkness, E.P., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N.H., Kirkness, E.P., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N.H., Kirkness, E.P., Weinstock, K.G., Gocayne, J.D., White

C.J., Lee, N.H., Fritchman, J.L., Gocayne, J.D., Fitzgerald

J.M., Fitzhugh, W.M., Fritchman, J.L., Gocayneson, N.S., Glodek, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M.,

Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Soctt, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hastings, G.A., He, W.W.,

Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,

Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,

Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Freser, C.M., and

Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                           CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT 266
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                                                                                                           LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40
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                                MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                                                                                                                                                                                                                                                                TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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CDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 410.

Location/Qualifiers
                                                                                                          AA581222 440 bp mRNA linear EST 05-JAN-1998 nd38e09.rl NCI CGAP CO1 Homo sapiens CDNA clone IMAGE:802600 5' similar to SW:LECG_CROAT P21963 GALACTOSE-SPECIFIC LECTIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrGlnArgSerGlnProlleTrplleGlyLeuHisAspProGlnLysArgGlnGlnTrp 105
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I (Dases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies Inc., David Krizman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAATTGCTATGGTTACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 HisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrileAlaGluTyrIleSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-rømail.nh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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Homo sapiens
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157 ArgPro 158
                                   420 CGACCA 425
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                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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//do_type="mRNA"
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//tissue_type="adenocarcinoma, cell line"
//tissue_type="adenocarcinoma, cell line"
//lab host="MIH_MGC_91"
//clone_lib="MIH_MGC_91"
//note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
//note="Organ: prostate; Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

8 a 235 c 245 g 220 t
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               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 968)
                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: DTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
k column: 09
High quality sequence stop: 672.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                AI791498 13-DEC-1999 nRNA linear EST 13-DEC-1999 ni23g10.y5 NCI_CGAP_CO4 Homo sapiens cDNA clone IMAGE:968898 5' similar to SW:LECG_CROAT P21963 GALACTOSE-SPECIFIC LECTIN. ;, mRNA
                               126 AsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThrTrpSerSerAsnGlu 145
                                                                                                                         310 AACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACTTGGAGCAGCAACGAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
TATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAGAAGAGGCAGCAGTGG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 526)
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This 5' resequenced clone has no previous 5' data to verify this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished
Other_ESTs: ni23g10.s1
Contact: Robert Straubberg, Ph.D.
                                                                                                                                                                       CysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                                                                               370 TGCAACAAGGCCCAACACTTCCTGTGCAAGTACCGACCA 408
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Insert Length: 1216 Std Error: 0.00
Seg primer: -40RP from Gibco
High quality sequence stop: 460.
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KEYWORDS
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141

BASE COUNT ORIGIN

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355
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                                                                                                                                                                                                                                                                  41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                                                                                                                               61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                                                                               296 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA
                                                                                                                                                                                                                             176 CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT
                                                                                                                                                                                                                                                                                    236 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT
                                                                                                                                          1 MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
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Length:
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Conservative:
Mismatches:
Indels:
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1.02e-75
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Human TSA7005 prot Human REG-like pro Human REG-like prot Human Colon tumour Human Colon specif Human Colon specif Human Colon specif

Human colon cancer Amino acid sequence speci Human Censer prote Human cancer speci Human zinc finger Sequence encoded b Sequence encoded b MUREG-1. Mus musc Rat reg protein. Rat reg protein (G Rat reg pr

OM protein

Run on:

Sequence:

Searched:

Database

Result No.

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New isolated colon specific gene - used to develop prods. for use in the diagnosis and treatment of colon disorders, partic. colon
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therapy; antibody; vaccine; agonist; antagonist.
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                                                                                                                        AAG75620
ABB99310
AAY92267
                                                                                                                                                             ABP76307
ABP59097
AAP81513
AAP83188
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ABP55369
ABP55370
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AAR59289
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AAR66595
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AAW18565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon specific protein.
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95WO-US07169
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N-PSDB; AAT51784.
                                                                       Homo sapiens
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· ** ** **
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A human Reg I-gamm
Human protein comp
Protein encoded by
Human colon specif
CS1-152 clone pred
CS80P similar amin
CS80P similar amin
                                                                                  December 31, 2003, 09:11:17; Search time 71 Seconds (without alignments) 353.223 Million cell updates/sec
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS1/gcgdata/geneseqy-emb1/AA41981.DAT:*
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          5.1.6
Compugen Ltd.
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          version 5
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Maximum Match 100%
Listing first 45 summaries
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AAW37929
AAW37866
AAW84274
AAB12900
AAM24517
AAM24517
AAM24519
                                                             sw model
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Gapop 10.0 , Gapext 0.5
          GenCore (c) 1993
                                                          protein search, using
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Maximum DB seq length: 200000000
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Human reg protein. Human colon associ Human cancer assoc

Human colon assoc:

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Length 158; Indels 9 9

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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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        The present sequence represents a human Reg I-gamma protein, which comprises a C-type lectin. The sequence was identified in Incyte clone 1310334. Reg I-gamma protein is involved in regulation of cell growth and development. Since the overexpression of reg proteins is associated with tumourogenesis and neurodegeneration, inhibition of human Reg i-gamma expression can be used for treating or preventing neoplasia or metastasis and neurodegenerative changes associated with Alzheimer's disease and other disorders of the central nervous system, e.g. Down's syntome. Reg I-gamma can also be used in therapeutics to induce regeneration of pancreatic beta-cells in the treatment of diabetes. The products can also be used for detection for, e.g. expression of REG I-gamma, diagnosis and drug screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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100.0%; Pred. No. 1.3e-84;
tive 0; Mismatches 0;
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(SAGA ) SAGAMI CHEM RES CENTRE.
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Matches 158; Conservative
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regulation; cell growth; development; tumourogenesis; neurodegeneration;
inhibition; treatment; prevention; neoplasia; metastasis;
neurodegenerative change; Alzheimer's disease; Down's syndrome;
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                                                                         A human colon specific protein (AAM12691) is a potential diagnostic marker for colon cancer. It is believed that the presence of active transcription of the colon specific gene in non-colon cells of a host is indicative of colon specific gene in non-colon cells sequence of the colon specific protein was deduced from a cDNA clone (AAT51784) isolated from a human colon cancer cDNA library. Recombinant colon specific protein can be produced in transformed host (e.g. bacterial, insect) cells and used to develop prods. for the diagnosis and treatment of colon disorders, partic. colon cancer metastasis. Antibodies raised against the protein can be used to target cancer cells and as part of a colon cancer vaccine.
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                                       Page 53; 64pp; English.
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cancer.
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ID AAW3
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Human protein comprising secretory signal amino acid sequence 3.
                                                                                     Human protein; secretory signal; nutritional source; cytokine; immunity; haematopoiesis; activin; inhibin; tumour; chemotactic; chemokinetic; thrombolytic; anti-inflammatory; inhibition;
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                                                                                                                                                                                                                                                                                     1 MASRSWRLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOS
                                                                                                                                                                                                                                                                 1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
This is the amino acid sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can be used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activin/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolysic activity, receptor/ligand activity, auti-inflammatory activity, tumour inhibition activity.
                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                Length 158;
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100.0%; Pred. No. 1.3e-84;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 158; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human colon specific polypeptides and polynucleotides for diagnosis and treatment of colon cancer, for screening compounds which interact with polypeptide, for synthesis of DNA and manufacture of DNA
                                                                                                                                         1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWPYHKSNCYGYFRKLRNWSDAELECOS
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                                                                                                             1 MASRSMRLLLLLLSCLAKTGVLGDIIMRPSCAPGWPYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon specific; colon cancer; metastasis; diagnose; treatment;
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Pred. No. 1.3e-84
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                                                       100.0%;
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158; Conservative
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polypeptides.
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YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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                                                                                                                                                                                                                                                                                                                                                                     Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer.
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                                                                                                                                     121. KSMGGNRCHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                 121 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                    CS1-152 clone predicted amino acid sequence.
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                                                                                                                                                                                                                                    AAM24517 standard; Protein; 158
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2000US-0480321.
2000US-0504629.
2000US-0519444.
2000US-0575251.
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, Wang T,
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               to AAI29512
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as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosotbant assay (ELISA)). AAI28460 to AAI299 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                               1 MASRSMRLLILLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                100.0%; Score 878; DB 22; Length 158; 100.0%; Pred. No. 1.3e-84; ive 0; Mismatches 0; Indels 0
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15-FEB-2000; 2000US-0504629.
06-WAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
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                                                                                             158 AA;
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GE, Wang T,
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                                                                                              Sequence
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activity of TCAPB by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (FCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity.

Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAM2494 to AAM24523 represent incleotide and amino acid sequences given in the exemplification of the present invention.
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15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0572251.
29-JUN-2000; 2000US-0609448.
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Colon tumor associated proteins and nucleic acids useful for the

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The present invention describes colon tumour associated proteins (1) and the polynucleotides (11) that encode them. (1) have cytostatic activity. (1) and (11) can be used in gene therapy and vaccine production. (1) and (11) and (11) and be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) compared to treat disorders associated with decreased expression by cativity of TCAPs by expressing inactive proteins or supplement the cativity of TCAPs by expressing inactive proteins or supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and the presence of similar nucleic acids in samples, and the presence of similar nucleic acids in samples, and the presence of similar nucleic acids in samples, and the assays to dentify modulators of TCAP expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate to the respective theorem and activity. The anti-(I) antibodies and antagonists may also be used to down regulate to the presence of an antibodies and antagonists may also be used to down regulate to the presence of cated the presence of TCAPs in samples.

TAP expression and activity. The anti-(I) antibodies may also be used to down regulate (E g. by enzyme linked immunosorbant assays (ELISA)). AA128460 to AA129512 and AAM34494 to AAM34523 represent invention.
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prevention, diagnosis and treatment of colonic cancer
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100.0%; Pred. No. 1.3e-84;
ive 0; Mismatches 0;
                                            Claim 2; Page 467-468; 472pp; English.
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Matches 158; Conservative
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10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
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The present invention describes colon tumour associated proteins (1) and the polynucleotides (11) that encode them. (1) have cytostatic activity. (11) may be used in the sene therapy and vaccine production. (1) and (11) and be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (1) and (11) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the proteints own production of them. Additionally, (11) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic glantitate the presence of similar nucleic acids in samples, and in assays to identify modulators of TCAP expression and activity. Anti-(1) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(1) antibodies may also be used as diagnostic agence for detecting the presence of TCAPs in samples.

TCAP expression and activity. The anti-(1) antibodies may also be used as diagnostic agence for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAMA4494 to AAMA4521 represent invention.
                                                                                                                                                                                                                                                         Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                         Stolk JA;
                                                                                                                                            Meagher MJ,
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19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
28-AUG-2000; 2000US-0649811.
                                                                                                                                                               King GE, Wang T, Jiang Y;
                                                                                           (CORI-) CORIXA CORP.
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                                                                                             1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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/ Match 100.0%; Score 878; DB 22; Local Similarity 100.0%; Pred. No. 1.3e-84; Nes 158; Conservative 0; Mismatches 0;
    Query Match
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Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer.
                                                                                                                          C880P similar amino acid sequence (GENESEQ W84274).
                             AAM24521 standard; Protein; 158 AA
                                                              AAM24521;
RESULT 10
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ID AAM
ID AAM
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100.0%; Score 878; DB 22;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 158; Conservative 0; Mismatches 0;
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                                                                                                                                  Secrist H,
                                                                              06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
                                                               10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629.
                                          29-DEC-2000; 2000WO-US35596
                                                                                                     28-AUG-2000; 2000US-0649811
                                                                                                                                          Jiang Y;
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                                                                                                                                  Xu J, Lodes MJ,
King GE, Wang T,
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Homo sapiens.
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RESULT 11

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YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for detecting REG-like protein (RELP) and its mucleic acid sequence. The method is useful for detecting the presence of a tumour. Kits comprising an antibody specific for RELP and reagents for detecting the antibody, or a nucleic acid complementary to a portion of a nucleic acid encoding RELP, are useful for identifying the presence of cancer, characterise the cancer, or monitor the course of treatment of cancer. The present sequence is human RELP protein used to illustrate the method of the invention. Human RELP gene is located at
                                                                                                                                                                                                                                                                                                                                                                         Detecting the presence of a tumor comprises detecting the concentration of a Reg Like Protein or the presence or quantity of a nucleic acid encoding it \, -
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genetic analysis, diagnostic, antisense therapy.
                                      23..158
/note= "Human mature REG-like protein"
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100.0%; Pred. No. 1.3e-84;
ive 0; Mismatches 0;
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 1..22
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding a polypeptide useful for the diagnosis and
                                                                                                                                                                 Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
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treatment of diseases associated with its expression -
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100.0%; Pred. No. 1.3e-84;
ive 0; Mismatches 0;
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                                                                                                                              Human TSA7005 protein SEQ ID NO:1.
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               AAB74934 standard; Protein; 158
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                                                                                         27-JUN-2001 (first entry)
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Length 158; Indels 9 9 120

RESULT 12

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The present sequence represents a new isolated REG-like protein (RELP) human immunoglobulin (Ig) derived protein. RELP comprises: (a) a human variable and connetant region, or (b) an isolated human Ig derived protein or specified portion or variant encoded by a nucleic acid. RELP has cytostatic activity and can be used as an Ig agonist and in protein threrapy. The RELP human Ig derived protein or a specified portion or variant can be used for preventing or treating a RELP protein mediated condition, malignant condition or disease condition, e.g. ancher. The nucleic acids can be used in producing RELP Ig derived chromosome 1p12-13.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated REG-like protein (RELP) human immunoglobulin derived protein or specified portion or variant, useful for preventing or treating a RELP protein mediated condition or malignant condition, e.g.
/label= signal
27..158
/label= RELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2; 101pp; English.
                                                                                                                                                                                                       14-MAR-2002; 2002WO-US07945
                                                                                                                                                                                                                                                          16-MAR-2001; 2001US-276305P.
                                                                                                                                                                                                                                                                                                            (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-103204/09.
N-PSDB; ABZ21635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 AA;
                                                                                                       WO200274916-A2
                                                                                                                                                       26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                               Heiskala M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed in cancer tissues. ABB78991 to ABB78004 represent proteins expressed in cancer tissues. ABB78991 to ABB78004 represent proteins cancoded by the ABB60775 to ABB78097 mucleic acid sequences. (1) can be encoded by the ABB60775 to ABB780047 mucleic acid sequences. (1) can be used in antiennse therapy. An antibody immunoreactive with a polypeptide encoded by (1) is useful for detecting cancer in a patient sample, and nucleic acid which hybridises to (1) in a cell. A probe/primer derived from (1) can be used for determining the presence of a pyridises to (1), and for determining the phenotype of cells in a sample of cells from a patient. (1) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (1) can be used to raise
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                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy -
                                                                                                                                                                               Catino TJ, Dwivedi P, Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analysis, mapping and diagnostic applications. (I) can be used tantibodies, and to screen for peptide analogues and antagonists.
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; Pred. No. 1.3e-84;
0; Mismatches 0;
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                                                                                                                                                                               Carroll E,
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                             02-OCT-2001; 2001WO-US30732.
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Matches 158; Conservative
                                                                                                                                                                               Burgess C, Astle JH, Ca
Thiaglingam A, Lewis ME;
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N-PSDB; ABQ60776.
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Best Local Similarity
                                                                                                                             (FARB ) BAYER CORP.
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                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer; tumour; immune response; immunostimulant; cytostatic; vaccine.
                                      ö
100.0%; Score 878; DB 24; Length 158; 100.0%; Pred. No. 1.3e-84; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon tumour protein for clone CS1-152 SEQ ID NO:1070.
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                                                                                                                                                                                                                                                                                                                                                      ABP55366 standard; Protein; 158 AA.
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Query Match
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Location/Qualifiers

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Search completed: December 31, 2003, 09:13:34 Job time : 72 secs

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- L3 ANSWER 58 OF 59 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN DUPLICATE 4
- AN 1993:432762 BIOSIS
- DN PREV199396087387
- TI A gene homologous to the reg gene is expressed in the human pancreas.
- AU Bartoli, Catherine; Gharib, Bouchra; Giorgi, Dominique; Sansonetti, Alice; Dagorn, Jean-Charles; Berge-Lefranc, Jean-Louis [Reprint author]
- CS Unite 315 l'INSERM, 46 Boulevard Gaye, 13258 Marseille Cedex 9, France
- SO FEBS (Federation of European Biochemical Societies) Letters, (1993) Vol. 327, No. 3, pp. 289-293.

 CODEN: FEBLAL. ISSN: 0014-5793.
- DT Article
- LA English
- OS Genbank-L08010
- ED Entered STN: 22 Sep 1993 Last Updated on STN: 6 Nov 1993
- AB We have determined the nucleotide sequence of reg1 a human genomic DNA fragment homologous to the reg gene which is expressed in the exocrine pancreas and regenerating islets. Sequence comparisons of reg and reg1 suggested similar exon-intron organisation. Based on this assumption, specific oligonucleotides for reg1 exons were used to demonstrate expression of the reg1 gene in pancreas and liver, The proteins encoded by reg and reg1 comprise 166 amino acids and differ by 22 amino acids only.

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rattus norv

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REG1 OR REG
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ID LITH RAT
AC P10758;
Best Local &
Matches 52
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::||||| ::|::| ::| ::| EEEDNVWIGLH-----HWNQARVWIDGSKKRYSAWDDDELPRGKYCTVLEGSSGFMSWE 116
                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
Lichostathine 1 precursor (Pancreatic stone protein 1) (PSP)
(Pancreatic thread protein 1) (PTP) (Islet of langerhans regenerating protein 1) (REG 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: EXPRESSED ONLY IN RECENERATING ISLETS AND NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS. EXPRESSED STRONGLY IN PANCREAS, MODERATELY IN GALLBLADDER, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unno M., Yonekura H., Nakagawara K.-I., Watanabe T., Miyashita H., Moriizumi S., Okamoto H., Itoh T., Terzoka H.;
"Structure, chromosomal localization, and expression of mouse reg genes, reg I and reg II. A novel type of reg gene, reg II, exists
                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 268:15974-15982(1993).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
CARBONATE PRECIPITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
LITHOSTAHINE 1.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POT
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SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                165 AA.
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PROSITE; PSSO041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=93340209; PubMed=8340418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00059; lectín c; 1.
PRINTS; PR01504; PNCREATITSAP.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                            (Rel. 32, Created)
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                                                143 SNECNKRQHFLCKY 156
                                                                   | |::| |:||
117 DNACSERNPFVCKY 130
                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Signal;
SIGNAL
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                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                              LIT1 MOUSE
P43137;
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                                                                                                                                               MOUSE
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29.0%; Score 254.5; DB 1; Length 165;

Query Match

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7;
                                                                                                                                               60 DLFCQNMNSG-YLVSVLSQAEGNFVASLIKESGTTDAN-VWTGLHDPKRNRRWHWSSGSL 117
                                                                                                                          55 ELECQSYGNGAHLASILSLKEASTIAEYI -- SGYQRSQPIWIGLHDPQKRQQWQWIDGAM 112
                                                           54
                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989 (Rel. 11, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Lithostathine precursor (Pancreatic atome protein) (PSP) (Pancreatic thread protein) (PPP) (Islet of langerhans regenerating protein) (REG) (Islet cells regeneration factor) (ICRF).
                                                           ---SCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                          8 ILLSCL-----IVLSPSQGQEAEEDLPSARISCPEGSNAYSSYCYYFTEDRLTWADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDIATE-91093273; PubMed=1985964;
MEDIATE-91093273; PubMed=1985964;
Rouguier S., Verdier J.M., Iovanna J., Dagorn J.-C., Giorgi D.;
"Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocrine cells, regulation by food content, and sequence identity with the endocrine reg transcript.";
J. Biol. Chem. 266:786-791(1991).
                             29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88115343; PubMed-2963000;
MEDLINE-88115343; PubMed-2963000;
Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y.,
Tochino Y., Okamoto H.;
Takasawa S., Shiga K., Yonemura Y.,
Tochino Y., Okamoto H.;
J. A novel gene activated in regenerating islets.";
J. Biol. Chem. 263:2111-2114(1988).
                                                                                                                                                                                           113 YLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKROHFLCKYR 157
                                                                                                                                                                                                              :
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                             Indels
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Yonekura H., Okamoto H.,
"Structure and characterization of rat Reg I gene.";
Selkagaku 65:1082-1082(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dusetti N.J., Frigerio J.M., Dagorn J.-C., Iovanna J.L., "Rapid PCR cloning and sequence determination of the rat
             1.4e-18;
thes 51;
             Pred. No. 1.4e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1174:99-102(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93326645; PubMed=7916640;
31.1%; Fic. 35;
                                                             10 LLLSCLAKTGVLGDIIMRP---
                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last seq
28-FEB-2003 (Rel. 41, Last anno
                             52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lithostathine gene."
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 22-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Pancreas;
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MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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009037;
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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 SDAELECQSYGNCAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYFILLSCL------MVLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 RLLLLLSCLAKTGVLGDIIMRPS------CAPGWFYHKSNCYGYFRKLRNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure, chromosomal localization and expression of mouse generencoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma."; Gene 185:159-168(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 GSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKWRDNSCDAQLSFVCKFK 164
                                                                                                                                                                                                                                                                                                                                                                                      . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.
Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
                                                                                                                                                                                                                                                                                                                                                                                                                               29.0%; Score 254.5; DB 1; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 3 precursor (REG III-gamma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Indels
 SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                   C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                      9B61EB236B82CF8A CRC64;
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BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas; MEDLINE=97208868; PubMed=9055810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 AA
                                                                                                                                                                                                                                                                                                                         LITHOSTATHINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Mismatches
                                                                                                                                                                                                    Incerpro; IPR001304; Lectin_C.
Interpro; IRR003909; Pancreatis_ac.
PEAM, PP00059; lectin_c; 1.
PRINTS; PR01504; PNCREATISAP.
SWART; SW00034; CLECT; 1.
PROSITE; PS06041; C_TVPE_LECTIN_1; 1.
PROSITE; PS60041; C_TVPE_LECTIN_2; 1.
Glycoprotein; Signal; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                    18672 MW;
                                                                                                                             EMBL; L07512; AAA41533.1; -.
EMBL; M62930; AAA41974.1; -.
                                                                                                                                                    EMBL; M18962; AAA42028.1; -.
EMBL; D26164; BAA0119.1; -.
PIR; A28351; A28351.
HSSP; P05451; 1LIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                           30.6%;
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                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 NGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDP----QKRQQWQWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| | | | | : | | | | : | | SG-HIVSVILSGAEASFLSSMIKSSGNSGQYVWIGLHDPTLGYEPNRGGWEWSNADVMNYI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLSCL-AKTGVLGDII-----MRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 MILISCLMLLSQVQGEVAKKDAPSSRSSCPKGSRAYGSYCYALFSVSKWYDADMACQKRP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSTE; PS00615; C.TYPE_LECTIN_1; FALSE_NEG.
PROSTE; PS00615; C.TYPE_LECTIN_2; 1.
Signal; Lectin; InflammaTory response; Acute phase; Multigene family.
Signal
1 26 POTENTIAL.
CHAIN 27 174 PANCREATITIS-ASSOCIATED PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 2 precursor (Lithostathine 3) (Islet of langerhans regenerating protein 3) (REG 3) (REG III-alpha).
                                                  -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL BACTERIAL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-TYPE LECTIN (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEALTHY PANCREAS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5575E9E56A4D8CEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .86-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas; MEDLINE=97208868; PubMed=9055810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.1%; Score 246.5;
35.2%; Pred. No. 9.8e
iive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P05451; 1LIT.
MGD; MGI:109406; Reg3g.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PP00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D63361; BAA18930.1; -. EMBL; D63362; BAA18931.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 35.2
les 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
170
162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 1
174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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us-09-525-041-2.rsp

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             Moriizumi S., Watanabe T., Unno M., Nakagawara K.I., Suzuki Y., Miyashita H., Yonekura H., Okamoto H.; Isolation, structural determination and expression of a novel reggene, human regI beta." Biochim. Biophys. Acta 1217:199-202(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                               characterization and possible pathophysiological implications.";
Eur. J. Biochem. 230:503-510(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION -!- PTHM. ALLO O-LINKED GIVCANS CONSIST OF GAL-GLCNAC-GAL-GALNAC TETRASACCHARIDE CORE AND GET ELONGATED (MICROHETEROGENEITY).
                                                                                                                                                                                                                                                                                                                                                                                                                     "The glycan moiety of human pancreatic lithostathine. Structure
                                                                                                                                                                           MEDLINE-93351647; PubMed-8348956;
Bartoli C., Gharib B., Giorgi D., Sansonetti A., Dagorn J.-C.,
Berge-Lefranc U.;
                                                                                                                                                                                                                                                                                                                                                                              De Reggi M., Capon C., Gharib B., Wieruszeski J.M., Michel R.,
                                                                                                                                                                                                                                              gene homologous to the reg gene is expressed in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00059; lectin_c; 1.

SMARY: SROUSO4; PROREATITSAP.
SMARY: SROO0615, CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Glycoprotein; Signal; Lectin, Pyrrolidone carboxylic acid.
SIGNAL
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 167771; -. GG, GO:0008283; P.cell proliferation; TAS. InterPro; IPR001304; Lectin C. InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                    CARBOHYDRATE-LINKAGE SITE.
MEDLINE=95331286; PubMed=7607222;
MEDLINE=94153997; PubMed=8110835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 BY
18665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D17291; BAA04124.1; -.
EMBL; D16616; BAA04091.1; -.
EMBL; L08010; AAA18204.1; -.
PIR; S34591; RGHU1B.
HSSP; P05451; 1LIT.
Genew; HGNC:9952; REGIB.
                                                                                                                                                                                                                                                                                        FEBS Lett. 327:289-293(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137
166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 167771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 NGAHLASILSIKEASTIAEYISG-YORSOPIWIGLHDPOKROO-----WOWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LLLSCLAKT-GVLGDIIM-----RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Lectin; InflammaTory response; Acute phase; Multigene family.
SIGNAL 1 26
BY SIMILARITY.
1 75
BY SIMILARITY.
DOWAIN 38 173
C-TYPE LECTIN (LONG FORM).
DISCULED 69 171
BY SIMILARITY.
DISCULPD 68 171
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Gaps
                       "Structure, chromosomal localization and expression of mouse genes
                                                                                     -i- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF BACTERIAL PROLIFERATION.
                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: SMALL INTESTINE, AND PANCREAS.
-!- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                  encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
Gene 185:159-168(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lithostathine 1 beta precursor (Regenerating protein I beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.6%; Score 242; DB 1; Length 175; 34.4%; Pred. No. 2.8e-17; ive 27; Mismatches 64; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 SWSG--KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3E311B3976E80F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Sont send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00615; C_TYPE_LECTIN 1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:109408; Reg3a.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00059, lectin c; 1.
PRINTS, PR01504, PNCREATITSAP.
SMART, SM00034, CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AA; 19539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, D63356; BAA18925.1; -.
EMBL, D63357; BAA18926.1; -.
EMBL; D63358; BAA18927.1; -.
HSSP; P05451; 1LTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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P48304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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87 QRSQP-IWIGLHDPQKRQQWQWIDGAMYLYRSW-SCKSMGGNK-HCAEMSSNNNFLTWSS 143
                                                                                                                                                                                                                                                                                                                                                               16
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                                                                                                                                                                                                                                                                                                                                                 33 RISCPEGTNAYRSYCYYFNEDPETWVDADLYCQNMNSG-NLVSVLTQAEGAFVASLIKES
LITHOSTATHINE 1 BETA.
C-TYPE LECTIN (LONG FORM).
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).

O-LINKED (GALNAC. .) (MUCIN TYPE).
BY SIMILARITY.
                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                 Length 166;
                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                       DIDC20E11AE5DDE8 CRC64;
                                                                                                                                                                                                                                 27.3%; Score 240; DB 1; 34.3%; Pred. No. 4.2e-17;
                                                                                                                                                                                                                                                                            27; Mismatches
                                                                                                                                              BY SIMILARITY
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61 RLTWGEADLFCQNM-NAGHLVSILSQAESNFVASLVKESGTTASN-VWTGLHDPKSNRRW 118
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                                         1 MASRSMRLLLLLSCLAKTGVLGDII-------MRPSCAPGWFYHKSNCYGYFRK
                                                                    48 LRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI -- SGYQRSQPIWIGLHDPQKRQQW
                                                                                                                                                                                                    106 QWIDGAMYLYRSWS--GKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 135
    72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: Contains 1 C-type lectin family domain. PIR; A38609; A38609. HSSP; P22897; LEGG. InterPro; IPR002353; Antifreezell. InterPro; IPR001304; Lectin C. InterPro; IPR00390; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TYPE LECTIN (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16291 MW; 04BAC45DB2B721C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.5%; Score 233; DB 1; 34.4%; Pred. No. 1.7e-16; ive 18; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
      33; Mismatches
                                                                                                                                                                                                                                                                                                                                               135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0615; C_TYPE_LECTIN_1; 1. PROSITE; PSSO041; C_TYPE_LECTIN_2; 1. Calcium; Lectin. 135 C-TYPE L. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00034; CLECT; 1.
      50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                            LECG CROAT
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CROAT
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Matches
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STDDSNVWIGLHDPKKARRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGFKKWKD 151
                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Lithostathine 2 precursor (Pancreatic stone protein 2) (PSP)
(Pancreatic thread protein 2) (PTP) (Islet of langerhans regenerating protein 2) (REG 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS AND NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS. EXPRESSED STRONGLY IN PANCREAS, WEAKLY IN LIVER, BUT NOT AT ALL IN GALLBLANDER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93340209; PubMed-8340418;
Unno M., Yonekura H., Nakagawara K.-I., Watanabe T., Miyashita H.,
Moriizumi S., Okamoto H., Itoh T., Teraoka H.;
"Structure, chromosomal localization, and expression of mouse reg
genes, reg I and reg II. A novel type of reg gene, reg II, exists
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 268:15974-15982 (1993).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 236.5; DB 1; Length 173; Pred. No. 9.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
LITHOSTATHINE 2.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                      173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97896; Reg2.
InterPro; IRR00233; Antifreezell.
InterPro; IRR001304; Lectin_C.
InterPro; IRR003999; Pancreatis_ac.
Pfam; PP00059; lectin_c; l.
RRINTS; PR01504; PNCREATITSAP.
PRINTS; SM00356; ANTIFREEZELI.
SMART; SM00014; CLECT; l.
PROSITE; PS50041; C_TYPE_LECTIN_1; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19407 MW;
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28.7%;
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HSSP; P05451; 1LIT.
                                                              144 NECNKRQHFLCKYR 157
                                                                                      | |: |:||::
|52 ESCEKKFSFVCKFK 165
                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the mouse genome.
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SIGNAL
                                                                                                                                                                                                      MOUSE
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SEQUENCE
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SOLUTION SERVICE SERVI

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61
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SUBUNIT: Homodimer; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dependent-type lectins.";
J. Biol. Chem. 266:2320-2326(1991).
-!- FUNCTION: Galactose-binding protein which recognizes specific carbohydrate structures and agglutinate a variety of animal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91115849; PubMed=1989986; Hirabayashi J., Kusunoki T., Kasai K.-I.; Harabayashi J., Kusunoki T., Kasai K.-I.; "Complete primary structure of a galactose-specific lectin from the venom of the rattlesnake Crotalus atrox. Homologies with Ca2(+)-
Galactose-specific lectin.
Crotalus atrox (Western diamondback rattlesnake).
Crotalus atrox (Western diamondback rattlesnake).
Evolutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
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DISULFIDE BOND
                                                                                        LITH BOVIN P23132;
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                                                                   RESULT
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62 GQENVWIGLERDKKKDFSWEWTDRSCTDYLTWDKNQPDHYQNKEFCVELVSLTGYRLMNDQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VALTTMSWMLLSSLMLLSQVQGEDAKEDVPTSRISCPKGSRAYGSYCYALFSVSKSWFDA 64
                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Gaps
                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley; TISSUE=Intestine;
MEDLINE=9406013; PubMed=8241280;
Frigerio J.-M., Dusetti N.J., Garrido P., Dagorn J.C., Iovanna J.L.,
"The pancreatitis associated protein III (PAP III), a new member of
the PAP gene family."; Acta 1216:329-331(1993).
-!- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
BACTERIAL PROLIFERATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PANCREATITIS-ASSOCIATED PROTEIN 3.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SCEDZE887C46E45C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.3%; Score 231; DB 1; Length 174; 32.4%; Pred. No. 3.5e-16; ive 28; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00615; C TYPE LECTIN 1; FALSE NEG. PROSITE; PS50041; C TYPE LECTIN 2; 1. Signal; Lectin; InflammaTory response; Acute phase. SIGNAL 1 26
                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pancreatitis-associated protein 3 precursor.
                                                                                                               174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S54979; S54979.
HSSP; P05451; 1LIT.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19143 MW;
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                                  ECNKROHFLCK 155
                                                       122 VČESKDAFLČO 132
                                                                                                               STANDARD;
                                                                                                                                                                                            Rattus norvegicus (Rat)
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38
40
68
145
174 AA;
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                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic thread protein) (PTP) (Islat of langerhans regenerating protein) (REG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=90368981; PubMed=2394826;
de la Monte S.M., Ozturk M., Wands J.R.;
"Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease and the developing human brain.";
J. Clin. Invest. 86:1004-1013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85298214; PubMed=3862086; Gross J., Brauer A.W., Bringhurst R.F., Corbett C., Margolies M. Gross J., Brauer A.W., Bringhurst R.F., Corbett C., Margolies M. "An unusual bovine pancreatic protein exhibiting pH-dependent globule-fibril transformation and unique amino acid sequence."; Proc. Natl. Acad. Sci. U.S.A. 82:5627-5631 (1985).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION.
                                      109 DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: CLEAVED TO GIVE AN A CHAIN AND A B CHAIN JOINED BY
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MEDLINE=91197388; PubMed=2085387;
Cai L., Harris W.R., Marshak D.R., Gross J., Crabb J.W.;
"Structural analysis of bovine pancreatic thread protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: IN PANCREATIC ACINAR CELLS.
                                                                                                                                                                                                                                        175 AA
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LITHOSTATHINE.
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Signal; Lectin.
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InterPro, IPR001304, Lectin_C.
InterPro, IPR003990, Pancreatis_ac.
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                                                                                                                                                                                                                                        STANDARD;
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EMBL; L10229; AAA02980.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 SYGNGAHLASILSLKEASTIAEYISGYQRSQ-PIWIGLHDPQKRQQ-----WQWIDGAMY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 KRPSG-HLVSVLSGAEESFVASLVRNNLNTQSDIWIGLHDPTEGSEANAGGWEWISNDVL 128
                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LLLSCLAKTGVLGDI -----IMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQ
                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
MEDLINE=93378971; PubMed=8369291;
Frigerio J.-M., Dusetti N.J., Keim V., Dagorn J.C., Iovanna J.L.;
Frigerio J.-M., Dusetti N.J., Keim V., Dagorn J.C., Iovanna J.L.;
Medentification of a second rat pancreatitis-associated protein.
Messenger RNA cloning, gene structure, and expression during acute pancreatitis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Secreted.
-!- SIBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: LOW EXPRESSION FOUND IN HEALTHY PANCREAS.
-!- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF PANCREATIC INFLAMMATION.
-!- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                       26.3%; Score 231; DB·1; Length 175; ilarity 30.9%; Pred. No. 3.5e-16; Conservative 30; Mismatches 62; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 LYRSW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 NYVAWETDPAAISSPGYCGSLSRSSGYLKWRDHNCNLNLPYVCKF 173
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MEDLINE-94314238; PubMed-8039722;
Suzuk; Y., Yonekura H., Watanabe T., Unno M., Moriizumi
Miyashita H., Okamoto H.;
"Structure and expression of a novel rat RegIII gene.";
Gene 144:315-316(1994).
           C-TYPE LECTIN (LONG FORM).
                                                                                                                                                  E -> FF (IN REF. 3).
C270EE70B7E91D6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Last sequence update) 28-FEB-2003 (Rel. 41, Last amnotation update) Pancreatitis-associated protein 2 precursor (Leg langerhans regenerating protein 3) (REG 3). PAP2 OR REG3.
                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
EE -> FF (IN REI
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173 C-
51 BY
171 BY
163 BY
85 EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sem
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   38 1
40
68 1
146 1
175 AA;
                                                                                                                                                                                                                                                                                                Similarity
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ID PAP2 RAT

AC 01-FEB-199

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86 YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 RISCPMGSKAYRSYCYTLVTTLKSWFQADLACQKRPSG-HLVSILSGGEASFVSSLVTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe T., Yonekura H., Terazono K., Yamamoto H., Okamoto H.; "Complete nucleotide sequence of human reg gene and its expression in normal and tumoral tissues. The reg protein, pancreatic stone protein, and pancreatic thread protein are one and the same product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LITA HUMAN STANDARD; PRT; 166 AA.
P05451; P11379;
01-NOV-1988 (Rel. 09, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Lithostathine 1 alpha precursor (Pancreatic stone protein) (PSP)
(Pancreatic thread protein) (PTP) (Islet of langerhans regenerating protein) (REG) (Regenerating protein I alpha) (Islet cells regeneration factor) (ICRF).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88115343; PubMed-2963000;
Terazono K., Yamamoto H., Takanawa S., Shiga K., Yonemura Y.,
Tochino Y., Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57; Indels
                                                                                                                                                                                                                                                                      PANCREATITIS-ASSOCIATED PRO
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W -> G (IN REF. 2).
                                                                                                                                                                                                                                       Acute phase
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J. Biol. Chem. 263:2111-2114(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                        26.0%; Score 228.5; DB 1
34.5%; Pred. No. 6.3e-16;
tive 25; Mismatches 57
                                                                                                                                                                                                                                   Signal, Lectin, Inflammatory response, Acu
SIGNAL 1 25 BY SIMILARITY
                                 PIR; A48689; A48689.
PIR; 160296; 183377.
HSSP; P05431; 1117.
Interbro; IPR001304; Lectin_C.
Interbro; IPR003990; Pancreatis_ac.
PEm; PP00599; Lectin_C; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                            PROSITE, PSO0615; C TYPE LECTIN 1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the gene.";
J. Biol.,Chem. 265:7432-7439(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90237042; PubMed=2332435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 LKWGDHHCDVELPFVCKFK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 LTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                  19599 MW;
D26078; BAA05071.1;
D23676; BAA04904.1;
                                                                                                                                                                             SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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172
50
170
162
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REDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross J., Carlson R.I., Brauer A.W., Margolies M.N., Warshaw A.L., Wands J.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 34-166.
MEDLINE-88029417; PubMed-3665916;
de Caro A.M., Bonicel J.J., Rouimi P., de Caro J.D., Sarles H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Partial amino acid sequence of human pancreatic stone protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Montalto G., Bonicel J.J., Multigner L., Rovery M., Sarles H.,
                                                                                                                                                              "Secretory pancreatic stone protein messenger RNA. Nucleotide sequence and expression in chronic calcifying pancreatitis."; J. Clin. Invest. 84:100-106(1989).
                                                                                               Giorgi D., Bernard J.-P., Rouquier S., Iovanna J., Sarles H., Dagorn J.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation, characterization, and distribution of an unusual pancreatic human secretory protein.", J. Clin. Invest. 76:2115-2125(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete amino acid sequence of an immunoreactive form of pancreatic stone protein isolated from pancreatic juice.", bir. J. Biochem. 168:201-207(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89150292; PubMed-2493268;
de Caro A.M., Adrich Z., Fournet B., Capon C., Bonicel J.J.
de Caro J.D., Rovery M.;
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       Boonyasrisawat W., Tandhanand-Banchuin N., Vannasaeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Biochem. J. 238:227-232(1986).
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MEDLINE=86086356; PubMed=3908481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87099950; PubMed=3541906;
                                                                  MEDLINE=89292148; PubMed=2525567;
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pancreas;
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                                                                                                                                                                                                                                                                                                                                                                                                             ALZHEIMER'S DISEASE AND DEVELOPMENTAL EXPRESSION REGULATION.
MEDILINE=90368981; PubMed=2294826;
de la Monte S.M., Ozturk M., Wanda J.R.;
"Enhanced expression of an exocrine pancreatic protein in Alzheimer's
disease and the developing human brain.";
J. Clin. Invest. 86:1004-1013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96256285; PubMed=8654365;
Bertrand J.A.; Pignol D., Bernard J.-P., Verdier J.-M., Dagorn J.-C.,
Fontecilla-Camps J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "What function for human lithostathine?: structural investigations by three-dimensional structure modeling and high-resolution NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- DEVELOPMENTAL STAGE: HIGH EXPRESSION LEVELS IN PETAL AND INFANT BRAINS, MUCH LOWER IN ADULT BRAINS.
-!- DISEASE: ALZHETMER'S DISEASE AND DOWN'S SYNDROME PATIENTS SHOW ENHANCED EXPRESSION OF PSP-RELATED TRANSCRIPTS AND INTRANBURONAL ACCUMULATION OF PSP-LIKE PROTEINS IN THEIR BRAINS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ontecilla-Camps J.C.;
Crystal structure of human lithostathine, the pancreatic inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.30 ANGSTROMS) OF 23-166.
MEDLINE=20092874; PubMed=10625646;
Gerbaud V., Pignol D., Loret E., Bertrand J.A., Berland Y.,
Fontecilla-Campa J.C., Canneslier J.P., Gabas N., Verdier J.M.;
"Mechanism of calcite crystal growth inhibition by the N-terminal undecapeptide of lithostathine.";
J. Biol. Chem. 275:1057-1064 (2000).
                                                                                                                                                                                                                                                                                 Itoh T., Tsuzuki H., Katoh T., Teraoka H., Matsumoto K., Yoshida Terazono K., Watanabe T., Yonekura H., Yamamoto H., Okamoto H.; "Isolation and characterization of human reg protein produced in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spectroscopy.";
Protein Eng. 9:949-957(1996).
-!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
--CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL.
SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION.
Rouimi P., Bonicel J., Rovery M., de Caro A.; "Cleavage of the Arg-Ile bond in the native polypeptide chain of human pancreatic stone protein."; FEBS Lett. 216:195-199(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NWR OF 34-164.
MEDLINE=97120677; PubMed=8961348;
Patard L., Stoven V., Gharib B., Bontems F., Lallemand J.-Y.,
de Reggi M.;
"What function for human lithostathine?: structural investigat
                                                                                                                                                                            "The human reg gene encodes pancreatic stone protein.";
Biochem. J. 260:622-623(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS)
                                                                                                                                                                                                                                                                MEDLINE=91032149; PubMed=2226837;
                                                                                                              IDENTITY OF REG WITH PSP.
MEDLINE=89350859; PubMed=2764894;
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EMBL; M27189; AAA60545.1; -.
EMBL; M18963; AAA36558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of stone formation.";
EMBO J. 15:2678-2684(1996).
                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 272:85-88(1990)
                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEVELS, IN BRAIN.
                                                                                                                                                                                                                                            DISULFIDE BONDS
                                                                                                                                                        Stewart T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16)
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    -!- SIMILARITY: Contains 1 C-type lectin family domain.

                                                                                                                                                                                                                                                                                                                                                                25.3%; Score 222.5; DB 1 34.3%; Pred. No. 2.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PAP OR PAPI OR HIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175
                                                                                                                                                                                                               SMART; SMO0034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Signal; G1ycoprofein.
                                                                                                                                      PIR, S32489, S32489.
HSSP, P20693, 1H1J.
InterPro, IPR001309, Pancreatis_ac.
InterPro, IPR003990, Pancreatis_ac.
                                                                                                                                                                                      Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                                                                                                                        20141 MW;
                                                                                                                            EMBL; X69062; CAA48800.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 SNECNKRQHFLCKY 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::: |:|||
153 DEHCDQKFPFICKY 166
                                                                                                                                                                                                                                                                                                                                                                                        46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                  93
65
156
172 AA;
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                  30
                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAP1 HUM
Q06141;
                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAP1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 SYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQOWOWIDGAMYLYRS 117
                                                                                                                                                                                                                                                                                                                                                                                                                  66 NINSSULTQAEGAFVASLIKESGTDDFN-VWIGLHDPKKNRRWHWSSGSLVSYKS 123
                                                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                                                                                                                                                                  LLLSCL-----AKTGVLGDI IMRPSCAPGWFYHKSNCYGYFRKLRNWSDABLECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pleurodeles lectin.";
Eur. J. Biochem. 213:901-907(1993).
-!- FUNCTION: MAY BE INVOLVED IN PROTECTION OF EGGS AND EMERYOS
AGAINST MICROORGANISMS. CALCIUM-DEPENDENT LECTIN WITH SPECIFICITY
TO D-GLUCOSE AND D-GLUCOSAMINE. CAN AGGLUTINATE MICROORGANISMS IN
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                        PROSITE; PSO0615; C_TYPE_LECTIN_1; 1.
PROSITE; PSS0041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Signal; AlZheiner's disease; Down's syndrome; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: ANTERIOR PART OF OVIDUCT.
MISCELLANEOUS: PROTEIN SYNTHESIS INCREASES SIGNIFICANTLY UNDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pleurodeles waltlii (Iberian ribbed newt).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae,
                                                                                                                     GO, GO:0008284; P:positive regulation of cell proliferation; TAS.
InterPro; IPR001253; Antifreezell.
InterPro; IPR001390; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PP00059; lectin_c; 1.
PRINTS; PR0150; PRCEATITSAP.
PRINTS; PR01556; ANTIFREEZEII.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                  th 25.7%; Score 225.5; DB 1; Length 166; Similarity 31.5%; Pred. No. 1.2e-15; 51; Conservative 30; Mismatches 62; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER (PROBABLE).
SUBCELLULAR LOCATION: SECRETED INTO THE INNER LAYER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Oviduct;
MEDLINE=93279340, PubMed=8504829;
Tiffeche C., Chesnel A., Jego P., le Pennec J.-P.;
"Isolation and characterization of a cDNA clone encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 21-34 AND 28-53
                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last seg
EMBL, J05412; AAA36559.1; -. EMBL; AR172331; AAD51330.1; EMBL, BC065350; AAH05350.1; PIR, A35197; RGHUIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESTRADIOL STIMULATION.
                                             PIR; A45751; A437.2..
PDB; 1LIT; 11-JAN-97.
PDB; 1QDD; 24-JAN-01.
Genew; HGNC:9951; REGIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lectin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8319;
                                                                                                  167770;
                                                                                                              167800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pleurodeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LECA PLEWA Q02988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
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                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                 Local
                                                                                    Genew; 16
                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 OP-IWIGLHDPOKROOWOWIDGAMYLY---RSWSGKSMGGNKHCAEMSSNNNFLT---WS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Pancreas, and Small intestine;
MEDLINE=93176807; PubMed=7679928;
Itoh T., Teracka H.;
"Cloning and tissue-specific expression of cDNAs for the human and mouse homologues of rat pancreatitis-associated protein (PAP).";
Biochim. Biophys. Acta 1172:184-186(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JUSSUE-Pancreas;
MEDLINE=93107309; PubMed=1469087;
Orelle B., Keim V., Masciotra L., Dagorn J.-C., Iovanna J.-L.;
"Human pancreatitis-associated protein. Messenger RNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LECTIN.
C-TYPE LECTIN (LONG FORM)
N-LINKED (GLCNAC. . .) (P.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
28B89FF12C136EA3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                            -!- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF PANCREATIC INFLAMMATION.
-!- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS AND IN SOME PATIENTS WITH CHRONIC PANCREATITIS.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                        Genomics 19:108-114(1994).
-!- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
BACTERIAL PROLIFERATION.
-!- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
                                                                                                                                                                                                                                                                                                                                                                                                ρě
                                                                                                                                                                                                                         Dusetti N.J., Frigerio J.M., Fox M.F., Swallow D.M., Dagorn J.C.
                                                                                                                                                                                                                                                          "Molecular cloning, genomic organization, and chromosomal localization of the human pancreatitis-associated protein (PAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANCREATITIS-ASSOCIATED PROTEIN 1.
C-TYPE LECTIN (LONG FORM).
                                                                                                                                                                                                                                                                                                                                                                            PANCREATIC ACINAR CELLS.
-!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE.
EXPRESSION IS FOUND IN HEALTHY PANCREAS.
                                                                                MEDLINE=92386513; PubMed=1325291;
Lasserre C., Christa L., Simon M.T., Vernier P., Brechot C.;
"A novel gene (HIP) activated in human primary liver cancer.";
Cancer Res. 52:5089-5095(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Y, CS1149FAC22EB68C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal, Lectin; InflammaTory response; Acute phase. SIGNAL 1 26 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G0:0005737; C:cytoplasm; TAS.
G0:0005615; C:extracellular space; TAS.
G0:0005625; C:soluble fraction; TAS.
G0:0005309; F:lectin; TAS.
G0:0007155; P:cell adhesion; TAS.
G0:0008283; P:cell proliferation; TAS.
G0:0007275; P:development; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
expression in pancreatic diseases.";
                Clin. Invest. 90:2284-2291(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                        MEDLINE=94245143; PubMed=8188210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D13510; BAA02728.1; --
EMBL; M84337; AAA36415.1; --
EMBL; S25768; AAB2642.1; --
EMBL; X68641; CAA48605.1; --
EMBL; L15533; AAA60020.1; --
EMBL; A46516; A49616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19395 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A49616; A49616.
HSSP; P05451; 1QDD.
Genew; HGNC:8601; PAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 AA;
                                                SEQUENCE FROM N.A.
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Iovanna J.L.
                                                                                                                                                                                       LISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DISULFID
DISULFID
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25.2%; Score 221; DB 1; Length 175;

Query Match

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                           .:
                                                                                                                                                 63 NGAHLASILSLKEASTIAEYISGYQRSQP-IWIGLHDPQKRQO-----WQWIDGAMYLYR 116
                                                                                                                                                                        3 SG-NLVSVLSGAEGSFVSSLVKSIGNSYSYVWIGLHDPTQCTEPNGEGWEWSSSDVMNYF 131
                                                                                         10 LLLSCL-AKTGVLGDIIMR--PS----CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DELL. J. Blochem. 266:352-358 (1999).
-!- FUNCTION: GALACTOSE-BINDING PROTEIN WHICH RECOGNIZES SPECIFIC CARBOHYDRATE STRUCTURES AND AGGLUTINATE A VARIETY OF ANIMAL CELLS BY BINDING TO CELL-SURFACE GLYCOPROTEINS AND GLYCOLIPIDS. MAY BE CALCIUM-DEPENDENT LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu Q., Wu X.-F., Xia Q.-C., Wang K.-Y..; "Cloning of a galactose-binding lectin from the venom of Trimeresurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- MISCELLANEOUS: Met-13 has been shown to be oxidized to methionine sulfoxide (Ref. 2) but this probably results from sample treatment prior to mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Venom;
PubMed=10561575;
Zeng R., Xu Q., Shao X.-X., Wang K.-Y., Xia Q.-C.;
"Characterization and analysis of a novel glycoprotein from snake
"Characterization chromatography-electrospray mass spectrometry and
Edman degradation.";
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Homodimer; disulfide-linked.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: Mw=17924.2; MW_ERR=2.4; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITE, AND STRUCTURE OF CARBOHYDRATES
                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
Galexbroad; (Rel. 41, Last annotation update)
Galactose-binding lectin precursor (TSL).
Trimeresurus stejnegeri (Chinese green tree viper).
Trimeresurus stejnegeri (Chinese green tree viper).
Lepidosauria; Squamata; Craniata; Vertebrata; Euteleostomi;
Viperidae; Crotalinae; Trimeresurus.
Viperidae; Crotalinae; Trimeresurus.
                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SEQUENCE OF 24-53, AND MASS SPECTROMETRY
                         64; Indels
                                                                                                                                                                                                                                  117 SW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKY 156
                                                                                                                                                                                                                                                           132 AWERNPSTISSPGHCASLSRSTAFLRWKDYNCNVRLPYVCKF 173
      Pred. No. 3.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                 PRT; 158 AA.
32.7%; Preα. ....
+ive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P22897; 1EGG.
Glycosultebb; 09YeB1, -- Lin.C.
InterPro; 1PR001304; Lectin.C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99348038; PubMed=10417338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stejnegeri.";
Biochem. J. 341:733-737(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF119097; AAD17252.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1.
                           53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
    Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANGE=24-158.
                                                                                                                                                                                                                                                                                                                                                                               LECG TRIST
Q9YGP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE,
                                                                                                                                                                                                                                                                                                                                        RESULT 15
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70 ILSLKEASTIAEYISGYQRSQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKSMGGNK- 127
                                                                                                                                                                                                                                                                                                                                                                                        6 FHRLAESLDIAEYISDYHKRQAEVWIGLLDRKKKDFSWEWTDRSCTDYLAWDKNQPDHYKD 125
                                                                                                                                                                                                                                                                                                                                 10 LLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLAS 69
                                                                                     GALACTOSE-BINDING LECTIN.
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLGNAC. . .) (HIGH MANNOSE).
/FIId=CAR_000165.
                                                                                                                                                                                                                                                                                  9; Gaps
                                                                                                                                                                                                                                                   Query Match
24.9%; Score 218.5; DB 1; Length 158;
Best Local Similarity 33.3%; Pred. No. 5.7e-15;
Matches 50; Conservative 19; Mismatches 72; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                               128 -- HCAEMSSNNNFLTWSSNECNKRQHFLCK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 KEFCVELVSLTGYHRWNDQVCESKNSFLCQ 155
PRINTS, PRO1504, PNCREATITSAP.
SMART, SM00034, CLECT; 1.
PROSITE, PRO0615, C.TYPE LECTIN 1; 1.
PROSITE, PS50041; C.TYPE LECTIN 2; 1.
Lectin, Signal, Calcium, Glycoprotein.
                                                                                                                                                                                                                        158 AA; 18635 MW;
                                                                       SIGNAL
CHAIN
DOMAIN
DISULFID
DISULFID
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CARBOHYD
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Search completed: December 31, 2003, 09:12:10 Job time : 39 secs

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Sequence

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Sequence

sequence 2, Appli sequence 1, Appli sequence 9, Appli sequence 6, Appli sequence 6, Appli sequence 1, Appli

Sequence 11, P Sequence 10, P Sequence 9, Ap

Sequence Sequence Sequence

Sequence Sequence

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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5180808-1
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US-08-410-530A-1
US-08-411-470-9
US-08-411-470-9
US-08-411-470-9
US-08-111-470-9
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Sequence 2, Application US/08729103

Sequence 2, Application US/08729103

Sequence 2, Application US/08729103

Sequence 2, Application US/08729103

SERREAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: GP INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
STATE: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
ADDIUM TYPE: Diskerte
COMPUTER: Diskerte
COMPUTER: IBM Compatible
OFBRATING SYSTEM: DOS
SOFTWARE: FASTSON Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DA
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  186.5
185.5
185.5
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172.5
171.5
170.5
168.5
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153.5
153
Command line parameters:
-MODEL=frame+ p2n, model - DEV=xlp
-MODEL=frame+ p2n, model - DEV=xlp
-QG-/CGMC_1USPTO spool p/US09525041/runat_31122003_091150_11891/app_query.fasta_1.327
-DG-/CGMC_2 I/USPTO spool p/US09525041/runat_31122003_091150_11891/app_query.fasta_1.327
-DG-/CGMC_2 I/USPTO spool p/US09525041/runat_shortsmenge_1 - LAOPCL=0
-LOSPEXT=0 - UNITS=bits - START=1 - SMD - 1 - MATRIX-blosume2 - TRANS-human40.cdi
-LIST-45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15
-WORELCAL - OUTPMT=pto - NORM=ext - HEAPSIZE=500 - MINLENEO - MAXLENE=200000000
-WORDELCAL - OUTPMT=pto - NORM=ext - HEAPSIZE=500 - MINLENEO - MAXLENE=200000000
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-NORMAP - LARGEQÜERY - NEG_SCORES=0 - WAIT - DSPELOCK=100 - LONGLOG
-DEV_TIMEOUT=120 - WARN TIMEOUT=30 - THRRADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 1, 8
Sequence 1, 8
Sequence 1, 8
Sequence 5, 8
Sequence 5, 8
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878
1 MASRSMRLLLLLSCLAKTGV......LTWSSNECNKRQHFLCKYRP 158
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Sequence 4,
Sequence 12,
Sequence 6,
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
   /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                         - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fotal number of hits satisfying chosen parameters:
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US-08-468-413-1
US-09-162-508-1
PCT-US95-07169-1
US-09-146-969-1
US-08-822-261-5
US-07-778-156-4
US-07-778-156-4
US-07-778-156-4
US-07-778-156-4
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US-07-778-156-4
US-07-778-156-4
US-07-778-156-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match
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Score

Result

Database :

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61
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 GluTyrIleSerGlyTyrGlnArgSerGlnProlleTrpIleGlyLeuHisAspProGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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Patent No. 5861494

GENERAL INFORMATION:
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: ROSELAND
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                  US-09-525-041-2 (1-158) x US-08-729-103-2 (1-614)
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOPTWARE: WORD PERFECT 5.1
                                                                                                                                                                                 7e-100
878.00
100.00%
100.00%
LENGTH: 614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLIGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: COLNFETO2
CLONE: 1310334
                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07068
                                                                                                                                                                  Alignment Scores:
                                                                                                                                 US-08-729-103-2
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US-08-468-413-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 AAGAGGCAGCAGTGGATTGATGGGCCATGTATCTGTACAGATCCTGGTCTGGC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09162508
Patent No. 6080722
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-525-041-2 (1-158) x US-08-468-413-1 (1-1114)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
APPLICATION NUMBER: US 08/468
FILING DATE: 06 JUN 95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.71e-99
878.00
100.00%
100.00%
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TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
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Best Local Similarity:
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111 ATGGCTTCCRGAAGCATGCGGCTGCTCTATTGCTGAGCTGCCTGGCCAAAACAGGAGTC 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                            141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro
                                                                                                                                                                                                APPLICANT: LI, ET AD.

TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07169
FILING DATE: 06 JUN 95
                                                                                                                                                          ; Sequence 1, Application PC/TUS9507169; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325,134
TELECHONE: 201-994-1704
TELECHONE: 201-994-1700
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878.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINEAR
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCT 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluTyr11eSerGlyTyrGlnArgSerGlnPro11eTrp11eGlyLeuHisAspProGln 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LeuGlyAspilelleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-525-041-2 (1-158) x US-09-162-508-1 (1-1114)
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDICATION DATA:
PREDICATION DATA:
PREDICATION DATA:
PTILING DATE: 06 JUN 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARC, GRECORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 35,800-447
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-994-1700
TELEFAX: 201-994-1704
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1114 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDENESS: SINGLE
                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,508
                                                                                    CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
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100.00%
100.00%
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US-09-162-508-1
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Best Local Similarity:
Query Match:
DB:
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Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPACIBLE
COMPUTER: PATEMINE PC-DOS/MS-DOS
SOFTWARE: PATEMINE PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,637
FILING DATE: 30-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REJERRENCE/DOCKET NUMBER: 2121-107P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-205-8050
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             Sequence 1, Application US/08464637
Patent No. 5834214
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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221.00
50.62%
32.72%
25.17%
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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HYPOTHETICAL: N
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                         121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
                            351 GACTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACGACGAG 410
                                                                     120
                                                                                                       470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                          101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
                                                                                                                                                                               471 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTAAACT
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                                                                                                                                                                                                                 141 TrpSerSerAanGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                                                                                                                             Sequence 1, Application US/09146969;
Patent No. 6228585;
GENERAL INFORMATION:
APPLICANT: Disckgraefe, Brian K.
TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury;
FILE REFERENCE: 04255.75314;
CURRENT APPLICATION UMBER: US/09/146,969;
CURRENT FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0;
LENGTH: 777
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445
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Matches:
Conservative:
Mismatches:
Indels:
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224.00
52.59%
33.33%
25.51%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                        RESULT 5
US-09-146-969-1
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APPLICANT: Invania, Juan-Lucio
APPLICANT: Dagorn, Jean-Charles
APPLICANT: Dagorn, Jean-Charles
APPLICANT: Barles, Jean-Charles
APPLICANT: Sarles, Jacques
TITLE OF INVENTION: Detection of Pancreatitis-Associated
TITLE OF INVENTION: Disease (as amended).

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 ---ProSer------CysAlaProGlyTrpPheTyrHisLysSerAsnCysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LeuleuleuSerCysleu---AlalysThrGlyValLeuGlyAspIleIleMetArg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreatitis-associated protein"
/note= "see, Fig. 3"
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Query Match
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53
29
64
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                    ATTORNEY JOATE:
NAME: Billings, Lucy J.
REGISTRATION UNDBER: 36,79
REFERENCE/DOCKET NUMBER: 9F-0251 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-85-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE:
                                                                                                                                                                                                                                                                                                               1.01e-18
221.00
50.62%
32.72%
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556 AAGTTC 561
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Best Local Similarity:
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IMMEDIATE SOURCE:
LIBRARY: GenBar
CLONE: 262368
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DB:
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Sequence 4, Application US/0778156; Patent No. 5436169; GENERAL INFORMATION:

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217 TCTGGA---AACCTGGTGTCTGTGTGTGTGGGGCTGAGGGATCCTTGTGTGTCCTCCTG 273
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                 APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                     ZIP: 22202
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,156
FILING DATE: 19911219
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Mismatches:
Indels:
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NAME: Oblon, No. 5436169man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 521-4500
TELEPAX: (703) 466-2347
TELEFX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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IOVANNA, JUAN-LUCIO
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50.31%
32.92%
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NUCLEIC ACID
EDNESS: unknown
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US-07-778-156-4
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Best Local Similarity:
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MOLECULE TYPE: c
ORIGINAL SOURCE:
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                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                  Alignment Scores:
Pred. No.:
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STATE: C.
COUNTRY:
   JS-08-822-261-5
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                               199 GCCTTGTTTTTGTCACCAAAATCCTGGACAGATGCAGATCTGGCCTGCCAGAAGCGGCCC 258
                                                                                   316 GTGAAGAGCATTGGTAACAGCTACTCATACGTCTGGATTGGGCTCCATGACCCCACACAG 375
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43 GlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSerTyrGly 62
                                                                  AsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAlaGluTyr 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 5, Application US/0882261
| Patent No. 5935813
| GENERAL INFORMATION:
| APPLICANT Hillman, Jennifer L.
| APPLICANT HILLMan, Jennifer L.
| TITLE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED
| TITLE OF INVENTION: PROTEIN
| NUMBER OF INVENTION: PROTEIN
| NUMBER OF SEQUENCES: 6
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Incyte Pharmaceuticals, Inc.
| STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE: Filed Herewith
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0251 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISOTRATION INTHREE: 36, 749
REFERENCE/DOCKET NUMBER: PF-0.
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                        155 LysTyr 156
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COUNTRY: L
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102 ArgGlnGln------TrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArg 116
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                                                                                                                                                                                                                                                                                                28 ---ProSer------CysAlaProGlyTrpPheTyrHisLysSerAsnCysTyr
                                                                                                                                                                                                                                                                                                                                                                                           43 GlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSerTyrGly
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Patent No. 6492499
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
797
23
29
16
                     Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE:
FILLING DATE:
                                                                                                                                                          US-09-525-041-2 (1-158) x US-08-822-261-5 (1-797)
                                                                                        Indels:
Length:
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Best Local Similarity:
Query Match:
DB:
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APPLICANT:
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                102 ArgGlnGln------TrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArg 116
                                               334 GCCACCGAGCCCAATGGAGAAGGTTGGGAGTGGAGTAGCAGTGATGAATTACTTT 393
                                                                                                   135 AsnAsnAsnPheleuThrTrpSerSerAsnGluCysAsnLysArgGlnHisPheleuCys 154
                                                                                                                                                                SerTrp-----SerGlyLysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSer 134
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: KEIM, VOLKER
APPLICANT: DAGONN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
AUBRES OF SEQUENCES. 12
CORRESSED SOLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
REGISTATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 ITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.02e-18
218.00
50.31%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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                                                                                                                                                                                                              Lys 155
                                                                                                                                                                                                                                              514 AAA 516
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TOPOLOGY: un)
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                           RESULT 10
US-08-422-166-4
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83 IleSerGlyTyrGlnArgSerGlnPro---IleTrplleGlyLeuHisAspProGlnLys 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 ArgGlnGln------TrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArg 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 GGCACCGAGCCCAATGGAGAAGGTTGGGAGTGGAGTAGCAGTGATGTGATGAATTACTTT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 SerTrp-----SerGlyLyBSerMetGlyGlyABnLyBHiBCyBAlaGluMetSerSer 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AsnAsnAsnPheteuThrTrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCys 154
                                                                                                                                                                                                                                                                       28 ---proSer------CyeAlaProGlyTrpPheTyrHisLy8SerAsnCysTyr 42
                                                                                                                                                                                                                                                                                                                                                                            43 GlyTyrPheArgLyBLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSerTyrGly 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 AsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAlaGluTyr 82
                                                                                                                                                                                                               37 ATGCTGCTTTCCTGCTGCTGCTGTCTCAGGTCAAGGTGAAGAACCCCAGAGGGAA 96
                                                                                                                                                                                                                                                                                                                                                                                                           157 GCCTTGTTTTGTCACCAAAATCCTGGACAGATGCAGATGCAGATGCAGAAGCGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                            10 LeuLeuLeuSerCysLeu---AlaLysThrGlyValLeuGlyAspIleIleMetArg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1755 Jefferson Davis Highway, Fourth Floor
     164
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
Mismatches:
Indels:
Gaps:
                                                                                                          US-09-525-041-2 (1-158) x US-08-422-166-4 (1-522)
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FILING DATE: 19911219
FILING SASSIFICATION: 435
CTTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5436169man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/07778156
Patent No. 5436169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IOVANNA, JUAN-LUCIO
KEIM, VOLKER
DAGORN, JEAN-CHARLES
32.92%
24.83%
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Arlington
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US-08-822-261-6
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GTGAAGAGCATTGGTAACAGCTACTTACGTCTGGATTGGGCTCCATGACCCCACACAG
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED
TITLE OF INVENTION: PROTEIN
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28
28
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Matches:
Conservative:
Mismatches:
Indels:
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                                 REFERENCE/DOCKET NUMBER: 354-012-0 PCT TELECOMMUNICATION INFORMATION: TELEPHONE: (703)521-4500
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Patent No. 5935813
GENERAL INFORMATION:
REGISTRATION NUMBER: 24,618
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218.00
50.31%
32.92%
24.83%
                                                                                                                        TELEEAX: (70) 486-2347
TELEEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE: pancreas
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Query Match:
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199 GCCTTGTTTTTGTCACCAAAATCCTGGACAGATGTGGAGAGTCTGGCCTGCCAGAAGCGGCCC 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 TCTGGA---AACCTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTGGTGTCCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 GGCACCGAGCCCAATGGAGAAGGTTGGGAGTGGAGTAGCAGTGATGATGAGTTACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LeuLeuLeuSerCysLeu---AlaLysThrGlyValLeuGlyAspileIleMetArg---
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53
28
64
16
                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE: Filed Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-525-041-2 (1-158) x US-08-822-261-6 (1-798)
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Matches:
           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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50.31%
32.92%
24.83%
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TYPE: nucleic acid
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CLONE: 189600
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Best Local Similarity:
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TOPOLOGY: line
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Pred. No.:
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199 GCCTTGTTTTTGTCACCAAAATCCTGGACAGATGCAGATCTGGCCTGCCAGAAGCGGCCC 258
                                                                                                                                                                                                                                                                                                                                                                                       376 GGCACCGAGCCCAATGGAGAAGGTTGGGAGTGGAGTAGCAGTGATGTGATTACTTT 435
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                                                                                                                                                                                                                                                                                                                                                                                                                            117 SerTrp-----SerGlyLyBSerMetGlyGlyAsnLyBHisCysAlaGluMetSerSer 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 AsnAsnAsnPheLeuThrTrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCys 154
                                                                                                                                       43 GlyTyrPheArgLysLeuArgAanTrpSexAapAlaGluLeuGluCysGlnSerTyrGly 62
                                                                                                                                                                                                             AsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAlaGluTyr 82
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 10 LeuLeuLeuSerCysLeu---AlaLysThrGlyValLeuGlyAspIleIleMetArg---
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                                                                   28 ---ProSer------CysAlaProGlyTrpPheTyrHisLysSerAsnCysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09146969
; Patent No. 6228585
; GENERAL INFORMATION:
; APPLICANT: Dieckgraefe, Brian K.
; TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
; TITLE OF INVENTION: UMBER: US/09/146,969
; CURRENT FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE PatentIn Ver. 2.0
; SEQ ID NO 2
LENGTH: 798
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US-09-146-969-2
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Pred. No.:
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135 AsnAsnAsnPheLeuThrTrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCys 154
                                                                                                                                                                                                                      Sequence 12, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS,
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/NS-LUOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
FELERENCE/DOCKET NUMBER: 354.618
REFIRENCE/DOCKET NUMBER: 354.012-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base paire
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Conservative:
Mismatches:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: unknown
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ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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Pred. No.:
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US-08-422-166-12
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                                                                                                                                               83 IleSerGlyTyrGlnArgSerGlnPro---IleTrpIleGlyLeuHisAspProGlnLys 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09226852
Patent No. 6492499
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN PANCEATITIS-ASSOCIATED TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DESCRIPTION OF STATEMENT SYSTEM: DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/226,852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-0251 U:
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
** TELEPAX: 415-845-4166
** INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
** TELEPAX: 415-845-4166
** INFORMATION FOR SEQ ID NO: 6:
** SEQUENCE CHARACTERISTICS:
** TENTY: 798 base pairs
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
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102 ArgGlnGln------TrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArg 116
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           Length:
Matches:
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Search completed: December 31, 2003, 10:41:06 Job time : 79 secs

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein December 31, 2003, 09:11:17; Search time 43 Seconds (without alignments) 353.364 Million cell updates/sec Run on:

US-09-525-041-2 878 Perfect score:

1 MASRSMRLLLLLSCLAKTGV......LTWSSNECNKRQHFLCKYRP 158 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	OI	A47148	A28351	878596	RGHU1B	B47148	183377	A38609	S54979	A37194	A48689	RGHU1A	A45751	S32489	A49616	JC7134	JC5058	A41719	JC2415	JC4690	JC5059	JC7105	JC4691	S29822	T46256	A54423	857653	A47267	B47267	JC4329
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	Score	254.5	254.5	241.5	240	236.5	236.5	233	231	231	228.5	225.5	224	222.5	221	206.5	203.5	203	202.5	202.5	200.5	196.5	196.5	194	193	193	191	189	185.5	185.5
	Result No.		7	m	4	S	y	7	80	თ	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56			29

Description by the protein precursor - rat

NyAlternate names: lithostathine
C;Species: Rattus norvegicus (Norvey rat)
C;Species: Rattus norvegicus (Norvey rat)
C;Accession: A28351; A39081; PL0147; S34618
R;Terzono, K.; Yamamoto, H.; Takaswa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto
R;Terzono, K.; Yamamoto, H.; Takaswa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto
A;Title: A novel gene activated in regenerating islets.
A;Reference number: A32704; MUD:88115343; PMID:2963000
A;Accession: A28351
A;Molecule type: mRNA
A;Residues: 1-165 <TER>

brevican precursor	neurocan precursor	agkisacutacin beta	asialoglycoprotein	aggretin alpha cha	hepatic lectin H1	chondroitin sulfat	neurocan - mouse	versican precursor	versican precursor	asialoglycoprotein	lectin BRA3-1 prec	lectin BRA3-2 prec	versican precursor	versican precursor	coagulation factor
S49126	S28764	JC7135	S13165	PC7027	LINHUL	A47171	S52781	A55535	A60979	LNHU2A	LNRC1	LNRC3	T14274	T42389	B42972
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883	1257	146	301	144	291	3562	1268	2397	2409	311	162	162	1643	3381	123
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	21.1	21.0	20.8	20.7	20.6	20.6	20.4	20.4	20.4	20.3	20.2	20.5	20.2	20.	19.6
	185 21.1		182.5 20.8			181 20.6									

ALIGNMENTS

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A47148

C;Species: Mus musculus (house mouse)
C;Accession: A47148

B;Unno, M.; Yonekura, H.; Nakagawara, K.; Watanabe, T.; Miyashita, H.; Moriizumi, S.; Oke J. Biol. Chem. 268, 15974-15982, 1993
A;Title: Structure, Chromosomal localization, and expression of mouse reg genes, reg I ar A;Reference number: A47148; MUID:93340209; PMID:8340418
A;Reference number: A47148
A;Status: preliminary
A;Molecule type: DNA
A;Status: 1-165 < UNN>
A;Cross-references: GB:D14010; NID:g391771; PIDN:BAA03111.1; PID:g391772
C;Genetics:
A;Introns: 21/1; 60/3; 106/3; 144/A
C;Superfamily: tetranectin; C-type lectin homology
F;35-161/Domain: C-type lectin homology < LCH>
F;35-46,63-161,136-153/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 DLFCQNMNSG-YLVSVLSQAEGNFVASLIKESGTTDAN-VWTGLHDPKRNRRWHWSSGSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 BLECOSYGNGAHLASILSLKEASTIAEYI -- SGYQRSQPIWIGLHDPQKRQQWQWIDGAM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LLLSCLAKTGVLGDIIMRP-----SCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 YLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.0%; Score 254.5; DB 2 Best Local Similarity 31.1%; Pred. No. 6.6e-18; Matches 52; Conservative 35; Mismatches 51
A47148
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Gaps

64

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A;Residues: 1-166 CBAR.
A;Residues: 1-166 CBAR.
A;Cross-references: GB:L08010; NID:g307368; PIDN:AAA18204.1; PID:g487726
A;Across-references: GB:L08010; NID:g307368; PIDN:AAA18204.1; PID:g487726
A;Note: this gene appears to be expressed in pancreas and liver
R;Moriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, K.; Suzuki, Y.; Miyashita, H.; Yone}
B;Amoriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, R.; Suzuki, Y.; Miyashita, H.; Yone}
A;Title: Isolation, etructural determination and expression of a novel reg gene, human re
A;Reference number: S42729; MUID:94153997; PMID:8110835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:D17291; NID:g474307; PIDN:BAA04124.1; PID:g474308; Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like cleav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Superfamily: tetranectin; C-type lectin homology
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: glycoprotein; lectin; pancreas; pyroglutamic acid
E;1-22/Domain: signal sequence #status predicted <SIG>
E;1-22/Domain: signal sequence #status predicted <MAT>
E;23-166/Product: regenerating islet lectin lbeta #status predicted <MAT>
E;34-166/Product: pancreatic stone protein #status predicted <MAT2>
E;35-166/Product: pancreatic stone protein #status predicted <MAT2>
E;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
E;27/Binding site: carbobydrate (Thr) (Covalent) #status predicted
E;33-34/Cleavage site: Arg-Ile (trypsin) #status predicted
E;36-47,64-162,137-154/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NyAlternate names: reg-related protein; regl-beta protein
N;Contains: pancreatic stone protein (PSP)
N;Contains: pancreatic stone protein (PSP)
N;Contains: pancreatic stone protein (PSP)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Aug-1995 #text_change 16-Jun-2000
C;Accession: 834591; 842729; Ā44712
R;Bartoli, C; Gharib, B.; Giorgi, D.; Sansonetti, A.; Dagorn, J.C.; Berge-Lefranc, J.L.
FEBS Lett. 327, 289-293; 1993
A;Title: A gene homologous to the reg gene is expressed in the human pancreas.
A;Reference number: 834591; MUID:93351647; PMID:8348956
                                                                                                                                                                                                                                                                                                                                                                                                     84 --SGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSW--SGKSMGGNKHCAEMSSNNNFL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 DGSGEGADGRVWIGLHRPAGSRSWRWSDGTAPRFASWHRTAKARRGGR-CAALRDEEAFT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 RISCPECTNAYRSYCYYFNEDPETWVDADLYCQNMNSG-NLVSVLTQAEGAFVASLIKES
                                                                                                                                                                                                                                                       27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGY
                                                                                                                                                                                                     30 CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI-----
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;Cross-references: GB:D16816; NID:g474305; PIDN:BAA04091.1; PID:g474306
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                                                                                                          11;
          Length 142;
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Pred. No. 1.8e-16;
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                                                                                                     Indels
     27.5%; Score 241.5; DB 2; 33.8%; Pred. No. 1.1e-16;
                                                                                                     56;
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                                                                                                     23; Mismatches
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Map position: 2p12-2p12
Introns: 22/1; 61/3; 107/3; 145/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 TWSSNECNKRQHFLCK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:: | :| |:||
124 SWAARPCTERNAFVCK 139
                                                                                                          46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 46; Conserv
                                                       Similarity
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          Query Match
                                                       Best Local
Matches 4
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F:35-161/Domain: C-type lectin homology <LCH>
F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
A;Cross-references: GB:M18962; NID:g206604; PIDN:AAA42028.1; PID:g206605
R;Rouquier, S.; Verdier, J.M.; Iovanna, J.; Dagorn, J.C.; Giorgi, D.
Siol. Chem. 266, 786-791, 1991
A;Title: Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocra A;Reference number: A39081; MUID:91093273; PMID:1985964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;Cross-references: EMBL:L07512; NID:g393208; PIDN:AAA41533.1; PID:g393209
3;Comment: This protein is found in pancreatic calculi of mammals. A peptide bond betwee orein into an insoluble protein at a neutral pH of 5.5 to 7.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gross-references: GB:M62930; GB:J05722; NID:g206462; PIDN:AAA41974.1; PID:g206463
R;Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovery, M.
Comp. Biochem. Physiol.1 B 93, 793-797, 1989
A;Title: Characterization in rat pancreatic juice of a protein homologous to the human
A;Reference number: PL0147; MUID:90031455; PMID:2680252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Experimental source: pancreas
Dusetti, N.J.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.
lochim. Biophys. Acta 1174, 99-102, 1993
Title: Rapid PCR cloning and sequence determination of the rat lithostathine gene.
Reference number: S34618; MUID:93326645; PMID:7916640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
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C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 20-Sep-1999
C;Accession: S78596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----CAPGWFYHKSNCYGYFRKLRNW
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F;5-16,33-138,113-130/Disulfide bonds: #status experimental
F;61,67/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:::||:||:||:|| GSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKWRDNSCDAQLSFVCKFK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Baernholdt, D.; Andersen, S.O.
submitted to the Protein Sequence Database, September 1998
A;Reference number: $78596
A;Accession: $78596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       introns: 21/1; 60/3; 106/3; 144/1; Superfamily: tetranectin; C-type lectin homology; Keywords: pyroglutamic acid; 1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.0%; Score 254.5; DB 2 30.6%; Pred. No. 6.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 1-142 - SAR5-
A; Experimental source: egg-shell
C; Superfamily: tetranectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 RLLLLLSCLAKTGVLGDIIMRPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: protein
Residues: 22-69 <ADR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-165 <DUS>
                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-165 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
Molecule type: DNA
                                                                                                                                                                                                                                                                                                     Status: preliminary Molecule type: mRNA
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Cispecies: Rattus norvegicus (Norway rat)
Cibate: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Aug-1999
Cipate: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Aug-1999
Cipacession: S54979; S43438
Ribusetti, N.J.; Frigerio, J.M.; Szpirer, C.; Dagorn, J.C.; Iovanna, J.L.
Biochem. J. 307, 9-16, 1995
A;Fitle: Cloning, expression and chromosomal localization of the rat pancreatitis-associal A;Reference number: S54979; MUID:95234061; PMID:7717998
A;Recession: S54979
A;Retaus: preliminary
A;Molecule type: DNA
A;Residuss: 1-174 < cUS>
A;Residuss: 1-174 < cUS>
A;Cross-references: EMBL:U09193; NID:9483931; PIDN:AAA79231.1; PID:9483932
A;Cross-references: EMBL:U09193; NID:9483931; DAGORN, J.C.; Iovanna, J.L.
B;Cross-references: EMBL:U09193; NID:9483931; PMID:9241280
A;Frigerio, J.M.; Dusetti, N.J.; Garrido, P.; Dagorn, J.C.; Iovanna, J.L.
B;Cross-references: EMBL:U09193; MUID:94060113; PMID:8241280
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                                                                                                                                                                                                                                                                               95 VNNNQDIWIGLHDPTMGQQPNGGGWEWSNSDVLNYLNWDGDPSSTVNRGNCGSLTATSEP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 SQP-IWIGLHDPQKRQQWQWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GQENVWIGLRDKKKKDPSWEWTDRSCTDYLTWDKNQPDHYQNKEFCVELVSLTGYRLWNDQ 121
                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 RISCPMGSKAYRSYCYILVIIKSWPQADLACQKRPSG-HLVSILSGGEASPVSSLVIGR
                                                                                                                                                                                                                                86 YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNP
                                                                              27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
       9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
26.5%; Score 233; DB 2; Length 13:
Best Local Similarity 34.4%; Pred. No. 7.2e-16;
Matches 45; Conservative 18; Mismatches 64; Indels
       56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     galactose-specific - western diamondback rattlesnake
       49; Conservative 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatitis-associated protein PAP-3 - rat
                                                                                                                                                                                                                                                                                                                                                                                 139 LTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 LKWGDHHCDVELPFVCKPK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 ECNKROHFLCK 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-174 <FRI>
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       Matches
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R;Suzuki, Y; Yonekura, H.; Watanabe, T.; Unno, M.; Moriizumi, S.; Miyashita, H.; Okamot

Gene 144, 315-316, 1994

A;Title: Structure and expression of a novel rat RegIII gene.

A;Reference number: 160296; MUID:94314238; PMID:8039722

A;Accession: 160296

A;Residuas; preliminary; translated from GB/EMBL/DDBJ

A;Residuas: 1-174 cRES>

A;Cross-references: GB:D23676; NID:9471157; PIDN:BAA04904.1; PID:9471158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s.; ox
                                                                                                                                                                                                                                                                                                                          reg II, regenerating islet cells - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Jun-2000
C;Accession: B47148
R;Unno, M.; Yonekura, H.; Nakagawara, K.; Watanabe, T.; Miyashita, H.; Moriizumi, S.; O;
J. Biol. Chem. 268, 15974-15982, 1993
A;Title: Structure, chromosomal localization, and expression of mouse reg genes, reg I.A;Reference number: A47148; MUID:93340209; PMID:8340418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 LRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQW 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 STDDSNVWIGLHDPKKNRRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGFKKWKD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQNNVYLILFLCLMFLSYSQGQVAEEDFPLAEKDLPSAKINCPEGANAYGSYCYYLIED 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MASRSMRLLLLLSCLAKTGVLGDII-------MRPSCAPGWFYHKSNCYGYFRK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regenerating protein III (reg III) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;MOlecule type: DNA
A;Residues: 1-173 <UNN>
A;Cross-references: GB:D14011; NID:g391773; PIDN:BAA03112.1; PID:g391774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 QWIDGAMYLYRSWS--GKSMGGNKHCAEMSSNNNFLTWSSNBCNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:D26078; NID:g471159; PIDN:BAA05071.1; PID:g471160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.9%; Score 236.5; DB 2; Length 173; 28.7%; Pred. No. 4.2e-16; ive 33; Mismatches 72; Indels 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Introns: 22/1; 68/3; 114/3; 152/1
A;Introns: 22/1; 68/3; 114/3; 152/1
C;Superfamily: tetranectin; C-type lectin homology
C;43-169/Domain: C-type lectin homology <ucn. class control of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.9%; Score 236.5; DB 2; 35.3%; Pred. No. 4.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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Superfamily: tetranectin; C-type lectin homology; 39-170/Domain: C-type lectin homology <LCH>
                                                                                                                      | |: |:||::
152 ESCEKKFSFVCKFK 165
                                                                      144 NECNKROHFLCKYR 157
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Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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A; Residues: 1-174 < RE2>
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Firigerio, J.M.; Dusetti, N.J.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
Biochemistry 32, 9236-9241, 1993
A;Title: Identification of a second rat pancreatitis-associated protein. Messenger RNA cl
A;Reference number: A48689; MUID:93378971; PMID:8369291
A;Accession: A48689
A;Extus: preliminary
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
                                                                                                                                                                                                                                                                      A;Cross-references: GB:L10229; NID:g409014; PIDN:AAA02980.1; PID:g409015 CS:Uperfamily: tetranectin; C-type lectin homology E;39-170/Domain: C-type lectin homology <LCH> F;39-50,67-170,145-162/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 LIWSSNECNKROHFLCKYR 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 48; Conserv
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A;Residues: 38-138;141-175 <CAI>
A;Residues: 38-138;141-175 <CAI>
C;Comment: The purified protein undergoes a reversible globule-fibril transformation and C;Comment: The purified protein undergoes a reversible globule-fibril transformation and C;Superfamily: tetranectin; C-type lectin homology
C;Reywords: disulfide bond; extracellular protein; pancreas
C;Reywords: disulfide bond; extracellular protein; pancreas
F;40-171/Pomain: C-type lectin homology <LCH>
F;141-175/Product: pancreatic thread protein chain B #status experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: A37194; A53897
R,de la Monte, S.M.; Ozturk, M.; Wands, J.R.
C,d.lin. Inrest. 86, 1004-1013, 1990
A;Title: Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease an A,Reference number: A37194; MUID:90368981; PMID:2394826
A;Cross-references: GB:L20869; GB:S67496; NID:g463279; PIDN:AAA41809.1; PID:g463280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 SYGNGAHLASILSLKEASTIAEYISGYQRSQ-PIWIGLHDPQKRQQ-----WQWIDGAMY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 KRPSG-HLVSVLSGAEESFVASLVRNNLNTQSDIWIGLHDPTEGSEANAGGWEWISNDVL 128
                                                                                                                                                                                                                                                                                                               54
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                                                                                                                                                                                                                                                                                                                                                                   5 VALITMSWMLLSSLMLLSQVQGEDAKEDVPTSRISCPKGSRAYGSYCYALFSVSKSWFDA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatic thread protein precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                            1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LLLSCLAKTGVLGDI-----IMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQ
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                                                                                                                                                                                                                                                   Gaps
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;Residues: 1-175 <DEL>;Cross-references: GBLNS9794; NID:g163648; PIDN:AAA30750.1; PID:g163649;
;Cross-references: GBLNS9794; NID:g163648; PIDN:AAA30750.1; PID:g163649;
Cai, L.; Harris, W.R.; Marshak, D.R.; Gross, J.; Crabb, J.W.
Protein Chem. 9, 623-632, 1990
;Title: Structural analysis of bovine pancreatic thread protein.
;Reference number: A53897; MUID:91197388; PMID:2085387
                                                                                                                                                                            Query Match 26.3%; Score 231; DB 2; Length 174; Best Local Similarity 32.4%; Pred. No. 1.5e-15; Matches 55; Conservative 28; Mismatches 73; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.3%; Score 231; DB 2; Length 175; 30.9%; Pred. No. 1.5e-15;
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                                                         A;Introns: 26/1; 65/3; 111/3; 153/1
C;Superfamily: tetranectin; C-type lectin homology
F;40-170/Domain: C-type lectin homology <LCH>
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N'Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; reg1-al N'Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; reg1-al N'Contains: pancreatic stone protein (PSP)
C) Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31-Mar-1990 #sequence revision 03-Aug-1995 #text_change 08-Dec-2000
C; Accession: A35197; B28351; $12950; S02767; S02419; S00113; S01471; A25246
R; Watanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.
J. Biol. Chem. 265, 7432-7439, 1990
A; Title: Complete nucleotide sequence of human reg gene and its expression in normal and product of the gene.
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A;Residues: 1.166 <WAT>
A;Residues: 1.166 <WAT>
A;Cross-references: GB-305412
R;Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto
J. Biol. Chem. 263, 2111-2114, 198
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A,Residues: 23-25.160-166 <-ITO>
A,Note: sequence determined from protein isolated after human cDNA sequence was cloned ar R;de Caro, A.M.; Adrich, Z.; Fournet, B.; Capon, C.; Bonicel, J.J.; de Caro, J.D.; Rover, Biochim. Blophyw. Acra 944, 281-284, 1989
A;Title: N-terminal sequence extension in the glycosylated forms of human pancreatic stor A;Reference number: S02767; MUID:89150292; PMID:2493268
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A; Residues: 1-166 <TRR>
A; Residues: 1-166 <TRR>
A; Cross-references: GB:M18963; NID:g190978; PIDN:AAA36558.1; PID:g190979
A; Cross-references: GB:M18963; NID:g190978; H.; Matsumoto, K.; Yoshida, N.; Terazono, BFBS Lett. 272, 85-88, 1990
FEBS Lett. 272, 85-88, 1990
A; Title: Isolation and characterization of human reg protein produced in Saccharomyces 64, Reference number: $12950; MUID:91032149; PMID:2226837
                                                                                                                                                                                                                                                                                                                                                                                                          S VNNNQDIWIWLHDPTWGQQPNGGGWEWSNSDVLNYLNWDGDPSSTVNRGNCGSLTATSEF 154
                                                                                                                                                                                                                                                                                                                                                 86 YQRSQPIWIGLHDPQKRQQ-----WQWIDGAMYLYRSWSG--KSMGGNKHCAEMSSNNNF 138
                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                      27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                    Gaps
                                                                                                9
ch 26.0%; Score 228.5; DB 1; Length 174; 1 Similarity 34.5%; Pred. No. 2.6e-15; 48; Conservative 25; Mismatches 57; Indels 9.
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A;Reference number: A35197; MUID:90237042; PMID:2332435
A;Accession: A35197
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FEBS Lett. 229, 171-174, 1988
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A, Residues: 23-47 <DEC>
R, Rouimi, P., de Caro, J.
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panoreatitis-associated protein PAP-2 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

RESULT 10

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pancreatitis-associated protein precursor - human Spancreatitis-associated protein pancreatitis at the man series ("Lype lectin; pancreatic stone protein homolog HIP Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cibate: 20-Feb-1995 #text_change 21-Jul-2000 C; Accession: A49616; A44931; $29821; $48197; I55580 R; Dusetti, N.J.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L. Genomics 19, 108-114, 1994 A; Title: Molecular cloning, genomic organization, and chromosomal localization of the hum A; Reference number: A49616; MuID:94245143; PMID:8188210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C;Accession: S32489; S28530
R;Tiffoche, C.; Chesnal, A.; Jego, P.; le Pennec, J.P.
Bur. J. Biochem. 213, 901-907, 1993
A;Title: Isolation and characterization of a cDNA clone encoding a Pleurodeles lectin.
A;Reference number: S32489; MUID:93279340; PMID:8504829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 GYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSW--SGKSMGGNKHCAEMSSNNNFLTWS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 GTDDFN-VWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYI--S
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                                                                                                                                                                              A;Cross-references: GB:M27190; NID:g623412; PIDN:AAA60546.1; PID:g623413 C;Superfamily: tetranectin; C-type lectin homology F;36-162/Domain: C-type lectin homology <LCH>
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A;Residues: 1-172 <TIF>
A;Cross-references: EMBL:X69062; NID:g64257; PIDN:CAA48800.1; PID:g64258
C;Superfamily: tetranectin; C-type lectin homology
F;37-164/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                           25.5%; Score 224; DB 2; Length 166; larity 33.3%; Pred. No. 7e-15; Conservative 26; Mismatches 58; Indels
                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-166 <GIO>
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151 DVPCEDKFSFVCKFK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 SNECNKROHFLCKYR 157
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153 DEHCDQKFPFICKY 166
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Matches 46; Conserv
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Best Local Similarity
Matches 45; Conserv
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A; Residues: 1-175 < DUS>
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A;Introns: 22/1; 61/3: 107/3; 145/1
A;Introns: 22/1; 61/3: 107/3; 145/1
C;Superfamily: tetranectri, C-type lectin homology
C;Superfamily: tetranectri, C-type lectin, pancreas; pyroglutamic acid
F;1-22/Domain: signal sequence #status predicted <SIG>
F;2-166/Product: regenerating islet lectin 1-alpha #status experimental <MAT>
F;34-166/Product: pancreatic stone protein #status experimental <MAT>
F;34-166/Product: pancreatic stone protein #status experimental <MAT>
F;35/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F;37/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;33-34/Cleavage site: Arg.Ile (trypsin) #status experimental
F;33-34/Cleavage site: Arg.Ile trypsin) #status experimental
A; Title: The disulfide bridges of the immunoreactive forms of human pancreatic stone pro A; Reference number: S02419; MUID:8815214; PMID:3345835
A; Accession: S02419
A; A; Rocession: S02419
A; Rocession: So2419
A; Roce
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A;Molecule type: protein
A;Molecule type: protein
A;Mostales: 33-48 <RO2.
R;Montalto, G. Bonicel, J.; Multigner, L.; Rovery, M.; Sarles, H.; De Caro, A.
Biochem. J. 238, 227-232, 1986
A;Title: Partial amino acid sequence of human pancreatic stone protein, a novel pancreat
A;Reference number: A25246; MUID:87099950; PMID:3541906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 34-166 <DE1>
A,Residues: 34-166 <DE1>
F,Rouimi, P.; Bonicel, J.; Rovery, M.; de Caro, A.
FEBS Lett. 216, 195-199, 1987
A,Title: Cleavage of the Arg-Ile bond in the native polypeptide chain of human pancreati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein A;A:0,7:89-98 cMON> A;Residues: 34-73,XV,75-89,'R', 89-98 cMON> C;Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like clea C;Comment: Intact regenerating islet lectin 1-alpha, lithostathine, inhibits the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expre
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C;Species: Homo sapiens (man)
C;Accession: A45751
R;Giorgi, D.; Bernard, J.P.; Rouquier, S.; Iovanna, J.; Sarles, H.; Dagorn, J.C.
J. Clin. Invest. 84, 100-106, 1989
A;Fitle: Secretory pancreatic stone protein messenger RNA. Nucleotide sequence and A;Feference number: A45751; MUID:89292148; PMID:2525567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 NWNSG-NLVSVLTQAEGAFVASLIKESGTDDFN-VWIGLHDPKKNRRWHWSSGSLVSYKS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 MLISCLMFLSQSQGQBAQTELPQ---ARISCPEGTNAYRSYCYYFNEDRETWVDADLYCQ 65
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Pred. No. 5e-15;
0; Mismatches 62; Indels 19,
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Matches 51; Conservative
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Length 172;

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122 SKKCLGVHIETGFHKWENFYCEQQDPFVCE 151
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Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homolog Reference number: 829821; MUID:93176807; PMID:7679928
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;Orelle, B.; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
;Orelle, B.; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
; Clin. Invest. 90, 2284-2291, 1992
; Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in Reference number: I55580; MUID:93107309; PMID:1469087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Vernir. J. Biochem. 224, 29-38, 1994
Title: Structural organization and chromosomal localization of a human gene (HIP/PAP)
Reference number: S48197; MUID:94357229; PMID:8076648
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                                                                                                                                                                                                                                            Cross-references: GB:X68641; NID:g312806; PIDN:CAA48605.1; PID:g312807; Experimental source: hepatocellular carcinoma Note: sequence extracted from NCBI backbone (NCBIN:113007, NCBIP:113008). Itoh, T.; Teraoka, H.
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Best Local Similarity 32.7%; Pred. No. 1.5e-14;
Matches 53; Conservative 29; Mismatches 64; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 26/1; 65/3; 111/3; 154/1
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: acute phase; extracellular protein; pancreas
F; 1-26/Domain: signal sequence #status predicted <SIG>
F; 27-175/Product: pancreatitis-associated protein #status predicted <MAT>
F; 40-171/Domain: C-type lectin homology <LCH>
F; 40-51, 68-171, 146-163/Disulfide bonds: #status predicted
;Cross-references: GB:L15533; NID:g482908; PIDN:AAA60020.1; PID:g482909; Lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C. ancer Res. 52, 5089-5095, 1992
ancer Res. 52, 5089-5095, 1992
ancer Res. 52, Anvel gene (HIP) accivated in human primary liver cancer.; Reference number: A44931; MUID:92386513; PMID:1325291
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.Cross-references: GB:S51768; NID:g262368; PIDN:AAB24642.1; PID:g262369
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Cross-references: GDB:136839; OMIM:167805
Map position: 2p12-2p12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: S48197
                                                                                                                                                                               Accession: A44931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom A;Reference number: JC7134; WUID:20025379; PMID:10558903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 IBSSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEE--- 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 ILSLKEASTIAEYISGYQRSQPI--WIGLHDPQKRQQW--QWIDGAMYLYRSWSGKSMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LILLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                           A;Accession: PC7037
A;Molecule type: protein
A;Rosidues: 24-53;84-86;87-94;125-136;137-152 <CH2>
A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Reywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SIG>
P;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 206.5; DB 2
Pred. No. 3.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 NYHCAEMSSNNNFLTWSSNECNKRQHFLCK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Mismatches
                                                                                                                                                                                           A,Residues: 1-152 <CHE>A,Cross-references: GB:AF176420
A,Experimental source: venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.5%;
31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.34
Matches 47; Conservative
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Search completed: December 31, 2003, 09:15:53 Job time : 44 secs

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December 31, 2003, 09:11:17; Search time 68 Seconds (without alignments) 599.593 Million cell updates/sec
                                                                                                                                US-09-525-041-2
878
1 MASRSMRLLLLLSCLAKTGV......LTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                             830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                              sp_archas:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mc:*
sp_organelle:*
sp_phage:*
sp_phage:*
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sp_unclassified:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_virus:*
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                              Sequence:
                                                                                                                                                                                                                               Searched:
                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9bvz8 homo gapien	O9d8q5 mus musculu	O9d858 mus musculu			Oscef9 mus musculu	O9psn0 bitis ariet	O8jiv9 aqkistrodon	Q9psm4 lachesis mu	Q9cvf4 mus musculu	O90wi8 bungarus fa	090wi7 bungarus fa	OBjiv8 aqkistrodon	090wi6 bungarus mu	O9psm8 echis carin	Q9dg39 agkistrodon
SUMMARIES	ΩI	Q9BYZ8	Q9D8G5	Q9D858	Q8NER7	QBNER6	QBC6F9	O9PSN0	Q8J1V9	Q9PSM4	Q9CVF4	G90WI8	Q90W17	QBJIVB	O90WI6	O9PSM8	Q9DG39
	8	4	11	11	4,	4	11	13	13	13	11	13	13	1	13	13	13
	Query Match Length DB	158	157	157	113	134	126	135	154	135	146	158	158	155	158	125	152
do	Query	100.0	68.4	67.7	62.0	35.0	26.8	26.7	26.3	26.1	25.9	25.9	25.9	25.2	24.4	24.3	24.1
	Score	878	600.5	594.5	544	307.5	235	234	230.5	229	227.5	227	227	221.5	214	213	211.5
	Result No.	1	~	9	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16

Lin W.-C.;
"Identification of gastrointestinal secretory protein (GISP), a new member of lithostathine gene family.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

TISSUE=Colon; Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases

SEQUENCE FROM N.A.

094931		091am1	QBjiwo	SAYGUS Ogdeao	ofn860	Q8jgt7		68806O	091840	QBjiv7	0988m5	Ognte7 homo sapien Oghbk4 homo sapien		OMO		Q8aya4 agki	Q9def8	081916		Birt Agreed	OBer 160	OBUVCE	Q8aya		ALIGNMENTS		158 AA.		- Fi	sequence update)	, mast ammotation update, (Gastrointestinal secretory protein GISP)	•		Craniata; Vertebrata; Euteleostomi; Catarrhini: Hominidae: Homo.					., Soares M.B.,	ng a nover member	1518:287-293 (2001).			Citadelle	., Citaliba2	involved in drug-resistance of	
09DG31	OSPAKE	O9IAM	QBJIW(OSYGN	098UJ	OBJGT	200	OPPSMS	Q9184	08JIV	098SM	O9HBK4	096FP7	Q96GW7	Q8TBB9	OBAYA4	OPDEF	OBJGT6	0011100	CALCAC	091AM(OBUVCE	QBAYAS	ì	Aric		PRT;			Last 66	Jastroir							111942;	id too a	in fami	287-29			Duggan] v E	a YTDE	gene is	
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146	152	152	152	154 155	146	158	15.00	131	146	146	124	911	911	911	911	146	146	146	316	140	146	158	158				PRELIMINARY;		ABLrel.	(TrEMBLrel.	type.	,	nan).	oa; Chordata; la: Primates:				Pubmec	charge h., bonald				ۇ ئۇنىي	Cancer;	. Lesuffleur T	lal Reg	
23.4	23.5	23.3	23.3	23.2	23.1	22.8		22.4		22.2				22.0								21.1	21.1						(TrE	(TrE	den (protein)	Hur H	ther	9096		N WC	10973	7 6	and ch	ophye	,	N W	Feer	Lesufi	testir	cella
17 205.5																										1 1	O9BYZ8	09BYZ8;	01-JUN-2001	01-JUN-2001	Regenerating	(REG-like p	Homo sapiens (Human)	Eukaryota; metazoa; Mammalia: Eutheria:	NCBI TaxID=	[1]	SEQUENCE FROM N.A.	MEDLINE=21210973; PubMed=11311942;	"Teolation and	the himan re	Biochim. Biophys. Acta	[2]	SEQUENCE FROM N.A.	Violette S	Lacasa M I	"The new int	colon tumor cells.";
н.	-1	10	0.0	N (V	2 2	60 (<i>A</i> C	. 6	7	m	M) C	n m	· m	m	m	m	mí	~) <	. 4	. 4	7	. 4.	4			RESULT	i	AC		בן ה		<u>D</u> B		38				X 6			Z.		85 C				RT

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Nature 409:685-690(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2010002L15RIK.
                                                               TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9D858
Q9D858;
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KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Erkunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Weltz C., Whittaker C., Wilming L.,

Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Wanshim-Parish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                                                                                                                                                      1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOS
                                                                                                                                                                                                                                                                                                                                                                                                                   1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
SEQUENCE FROM N.A.

A Kamarainen M., Heiskala K., Heiskala M., Andersson L.C.;
A Kamarainen M., Heiskala K., Heiskala M., Andersson L.C.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY007243, AAG02562.1;
REMBL; AY167243, AAG12569.1;
REMBL; BC017089; AAH17089.1;
REMBL; AF254415; AAH17089.1;
REMBL; AF254415; AAK8435.1;
REMBL; AF25415; AAK8435.1;
REMBL; AY16750; IPR001304; Lectin C.
RICEPPRO; IPR001304; Lectin C.
RICEPPRO; IPR001304; Lectin C.
RICEPPRO; IPR001309; Pancreatis ac.
                                                                                                                                                                                                                                                                                                                         100.0%; Score 878; DB 4; Length 158; 100.0%; Pred. No. 3.8e-87; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            POTENTIAL.
7308849CBBD6E93E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-JUAR-2003 (TrEMBLrel. 23, Last annotation update)
2010002115Rik protein (RIKEN cDNA 2010002115 gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 AA.
                                                                                                                                                                                                  Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                            SEQUENCE 158 AA; 18230 MW;
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0°
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                 Signal.
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XX STRAIN=C57BL/61; TISSUB=Small intestine;
XX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
XA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
XA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
XA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
XA Kadota K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,
XA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
XA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Allake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Allake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Anchone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,
XA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
XA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
XA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 YGNGSHLASVLNQKEASVISKYITGYQRNLPVWIGLHDPQKKQLWQWTDGSTNLYRRWNP 119
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                              Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AK008049; BAB25429.1; -.
EMBL, BC019465; AAH19465.1; -.
HSSP; P05451; 1QDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT: CTYPE LECTIN 2; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
SEQUENCE 157 AA; 18398 WW; F3981722BBD83968 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1914959; 2010002115Rik.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                        SEQUENCE FROM N.A.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                    Kamarainen M., Heiskala K., Heiskala M., Andersson L.C.; "RELP, a novel human REG-like protein."; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY126572; AAM95500.1; -SEQUENCE 134 AA; 14993 MW; EOESAD9B96A53EB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9PSNO;
01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE-Pancreas; MEDLINE=22354683; PubMed=12466851;
   REG-like protein splice variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 55.9
Matches 62; Conservative
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                                          Homo sapiens (Human)
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121 VCKFK 125
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE
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QBC6F9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.7%; Score 594.5; DB 11; Length 157; Best Local Similarity 65.6%; Pred. No. 1.9e-56; Matches 103; Conservative 25; Mismatches 28; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kamarainen M., Heiskala K., Heiskala M., Andersson L.C.;
"RELP, a novel human REG-like protein.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX126671; AAMS5599.1;
InterPro; IPR001304; Lectin C.
Interpro; IPR00390; panoreatis_ac.
Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
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InterPro; IRR001304; Lectin_C.
InterPro; IRR001390; Pancreatis_ac.
Pfan; PF00059; lectin_c; 1.
PRINTS; PR01504; PRCEATITSAP.
SMART; SM0034; CLECT; 1.
PR051TE; PS0041; C_TYPE LECTIN_2; 1.
SEQUENCE 157 AA; 18474 MW; PD96F36CFB989368 CRC64;
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SEQUENCE 113 AA; _1283Z MW; A2E9DF1A729C78DA CRC64,
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Last sequence update)
Last annotation update)
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Last annotation update)
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EMBL; AK008438; BAB25669.1; -.
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(TrEMBLrel. 22,
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Matches 101; Conservative
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01-OCT-2002
01-OCT-2002
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QBNER6;
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08NER7
1D 08NE 01-0
DT 01-0
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Q8NER6
ID Q8NE
AC Q8NE
DT 01-0
DT 01-0
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95 GLHDPQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNPLTWSSNECNKRQHF 152
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                                                                                                                                                          26
                                                                                                                                                                                               1 MASRSMRLLILLISCLAXTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAEVRNLL 60
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EMBL; AK075798; BAC35967.1; -.
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                                                                                                                                                      1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAEL----
                                                                              31; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                              61 PAWPGLSRAKDQPEPQ------ISFDSGSSV---LPGHYEEKPLWL 97
                                                                                                                                                                                                                                                                                                     57 ------ECQSYGNGAHLASILSLKEASTIAEYISGYQRSQPIWI 94
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35.0%; Score 307.5; DB 4; Length 134; 55.9%; Pred. No. 2e-25; tive 9; Mismatches 9; Indels 31
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotati
Regenerating islet-derived 1 (Fragment).
Mus musculus (Mouse).
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EMBL; AY091759; AAM22787.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GQAEVWIGLWDKKKDFSWEWTDRSCTDYLTWDKNQPDHYQNKEFCVELVSLTGYRLWNDQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NCPPDWLPMNGLCYKIFDELKAWEDAERFCRKYKPGCHLASFHQYGESLEIAEYISDYHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang W.-J., Ling Q.-D., Huang T.-F.; "Molecular structure and functional characterization of agglucetin, a tetrameric glycoprotein 1b-binding protein, from Formosan pit viper."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang W.J., Huang T.F.;
"A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist.";
Thromb. Haemost. 86:1077-1086(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                       29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGYOR
                                                                                                                                           MEDLINE-96161481; PubMed=8593494;
Nikai T., Suzuki J., Komori Y., Ohkura M., Ohizumi Y., Sugihara H.;
"Primary structure of the lectin from the venom of Bitis arietans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-type lectin (Agglucetin-alpha 1 subunit precursor)
Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Etteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Deinagkistrodon.
                                   Bitis arietans (African puff adder).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Viperinae, Bitis.
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Yu H., Xiang K., Wang Y., Liu J.;
"Member of C-type lectin family from Deinagkistrodon acutus.";
submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            26.7%; Score 234; DB 13; Length 135; 35.1%; Pred. No. 1.9e-17;
                                                                                                                                                                                (puff-adder).";
Biol. Pharm. Bull. 18:1620-1622(1995).
HISPS: P22897; 1EGG.
InterPro: IPR001304; Lectin_C.
InterPro: IPR001309; Pancreatis_ac.
Pfam; PF00059; lectin_c; 1.
PRINTS: PR01504; PNCREATITSAP.
SWART: SW00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                            46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 ECNKRQHFLCK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 VCGSKNAFLCQ 132
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                    NCBI_TaxID=8692
                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GHLVSIESAGERDFVAQLVSENKQTDNVWLGLKIQSKGQQCSTEWTDGSSVSYENFSEYQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 SFGLLVVFLSLSGTG--ADV----DCLPGMSAYDQSCYRVFKLLKTWDDAEKFCTERPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 SWRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Lachesis.
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                                                                                                                                                                                                                                                                                                                                                           26.3%; Score 230.5; DB 13; Length 154; 32.7%; Pred. No. 5.2e-17; ive 24; Mismatches 70; Indels 11;
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                                                                                                                                                                                                                                                                           24 154 AGGLUCETIN-ALPHA 1 SUBUNIT.
154 AA; 17317 MW; AA08E518S01BECC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Pancreatis_ac.
Pfam, PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSTITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSTITE; PS00615; C_TYPE_LECTIN_1; 1.
SEQUENCE 135 A4; _16223 MW; DSE9083A065A8F56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ---SKKCFVLEKNTGFRTWLNLNCGSEYAFVCKSPP
EMBL; AF540645; ANN23124.1; -.
InterPro; IRR001304; Lectin C.
InterPro; IRR001304; Lectin C.
Ffam; PR00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SWART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_1; 1.
Lectin; Signal.
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MEDLINE=97000492; PubMed=8843577;
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                                                                                                                                                                                                                                                                                                                                                                                                                    51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stenophyrs venom.";
Toxicon 34:763-769(1996).
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154
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Matches 51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P22897; 1EGG.
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Q90WI7
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SEQUENCE FROM N.A.

SEQUENCE TRON N.A.

SEQUENCE TRON D. Bubmed=11217851;

MEDINEZ-21085660; Pubmed=11217851;

MAZAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Azawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

B. Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

B. Aizawa T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

B. Aizawa T., Lewis S., Mareno Y., Nikaido I., Pesole G., Quackenbush J.,

R. Redota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

R. Chriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

B. Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

B. Sakai K., Okido T., Fletcher C., Fujita M., Gariboldi M.,

B. Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

B. Hordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

R. Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

B. Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

B. Ansachiasi V.,

B. B. A., Yoshida K., Raegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 VDNYQDIWIGLHDPTWGQQPNGGGWEWSNSDVLNYLNWDGDPSTVNRGHCGSLTASSGF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Rat generating islet-derived, mouse homolog 3 alpha (Fragment)
REG3A.
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25.9%; Score 227.5; DB 11; Length 146;
Best Local Similarity 34.5%; Pred. No. 1e-16;
Matches 48; Conservative 25; Mismatches 57; Indels 9;
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SEQÜENCE 146 AA; 16161 MW; 76D73B81BECC5FB1 CRC64;
                                                                                                                   146 AA.
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InterPro; IPR001304; Lectin_C.
InterPro; IPR0013990; Pancreatis_ac.
Pfam; PP00059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; PS00014; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
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                             122 VCESKNAFLCQ 132
 145 ECNKRQHFLCK 155
                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                           RESULT 10
Q9CVF4
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RESULT 11

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89 SQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGYQR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zha H.-G., Zhang Y.: "CDNA cloning and characterization of C-type lectin-like proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zha H.-G., Zhang Y.; "cDNA cloning and characterization of C-type lectin-like proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
01-MAR-2003 (TrEMBLrel. 21, Last annotation update)
C-type lectin-like protein 1.

Bungarus fasciatus (Banded krait).

Bungarus fasciatus (Chordets, Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-type lectin-like protein 2.

Bungarus fasciatus (Banded Krait).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Elapidae; Bungarinae; Bungarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.9%; Score 227; DB 13; Length 158; Best Local Similarity 33.6%; Pred. No. 1.3e-16; Matches 44; Conservative 22; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elapidae snakes.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 158 AA; 18638 MW; ECF85936FA4182B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF354270; AAK43584.1; -. InterPro; IPR001304; Lectin C.
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PRINTS; PR00556; ANTIFREEZEII.
PRINTS; PR01504; PNRRATITSAP.
SMART; SM00034; CLECT; 1.
PRELIMINARY;
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Venom gland;
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TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                     Elapidae snakes.";
                                                                                                                                                                                                                                  NCBI_TaxID=8613;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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                                                                                                                                                                                           70 ILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKSMGGNKHC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 IHSREEEAFVGKMASRTLKYTSMWLGLNNPWKECKWEWSDDTRLDYKVWTRR-----PYC 119
                                                                                                                                                                             89 SQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKSMGGNK---HCAEMSSNNNFLTWSSN 144
                                                                                                                       29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLAS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                 25 TCPIDWLPKNGLCYKVFSNPKSWLDAEMFCRKFKPGCHLASIHRDADSADLAEYVSDYLK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu H., Xiang K., Wang Y., Liu J.;
"Member of C-type lectin family from Deinagkistrodon acutus.";
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AYO91760; AAM227881;
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.2%; Score 221.5; DB 13; Length 155; 29.7%; Pred. No. 5e-16; tive 28; Mismatches 65; Indels 11;
                                                                25.9%; Score 227; DB 13; Length 158; 32.1%; Pred. No. 1.3e-16; ive 26; Mismatches 59; Indels 4
                                        18254 MW; 5F0218970DA17453 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 155 AA; 17944 MW; 3E935FF53773AB94 CRC64;
                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                155 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PRCEATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
                                                      Query Match
Best Local Similarity 32.13
Best Local Similarity 32.13
Conservative
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                                          158 AA;
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              PROSITE;
                                        SEQUENCE
  PROSITE;
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Matches
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Q8JIV8
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158 AA

01-DEC-2001 (TrEMBLrel. 19, Created)

PRELIMINARY;

Q90WI6;

9IM060

RESULT 14 Q90WI6 ID Q9 AC Q9 DT 01

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89 SQ-PIWIGLHDPOKRQQWQWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S GRGHVWIGLRDTKKKYIWEWIDRSRIDFLPWRKNQPDHFNNNEFCVEIVNFIGYLQWNDD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR 88
                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUBE-become juland; The subsequence juland; The H.-G., Zhang Y., "CDNA Cloning and characterization of C-type lectin-like proteins from "CDNA cloning and characterization of C-type lectin-like proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
C-type lectin-like protein 1.

Bungarus multicinctus (Many-banded krait).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Elapidae; Bungarinae; Bungarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
ECLV IX/X-BP beta SUBUNIT=CA(2+)-dependent coagulation factor
IX/factor X-binding protein beta subunit.
IX/factor X-binding protein beta subunit.
Euchis carinatus (Saw-scaled viper).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96196635; PubMed=8611513;
Chen Y.L., Tasi I.H.;
"Functional and sequence characterization of coagulation factor
IX/factor X-binding protein from the venom of Echis carinatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.4%; Score 214; DB 13; Length 1 32.1%; Pred. No. 3.3e-15; ive 22; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                            Elapidae snakes.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00059; lectin_c; 1.
SMARY; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 125 AA; 14372 MW; EDFEC2E49686CDD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 AA; 18706 MW; 66B71A29D1048805 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSO0615; C_TYPE_LECTIN_1; 1. PROSITE; PSSO041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
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HSSP; P23807; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                                         EMBL; AF354272; AAK43586.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 ECNKRQHFLCK 155
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Gaps
Query Match
24.3%; Score 213; DB 13; Length 125;
Best Local Similarity 32.5%; Pred. No. 3.2e-15;
Matches 41; Conservative 18; Mismatches 61; Indels 6
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¹⁵⁰ QHFLCK 155 ||:|| 116 GHFVCK 121

Search completed: December 31, 2003, 09:14:57 Job time : 70 secs

OPASU NINALE BLANK (USPTO)

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Minimum DB Maximum DB

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Searched:

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Sequence 1073, Appsequence 1073, Appsequence 1074, Appsequence 1074, Appsequence 1074, Appsequence 1074, Appsequence 1074, Appsequence 1074, Appsequence 1071, Appsequence 1072, Appsequence 1072, Appsequence 1069, Appsequence 1069, Appsequence 1069, Appsequence 1069, Appsequence 1069, Appsequence 1069, Appsequence 1072, Appsequence 1069, Appsequence 2117, Appsequence 2117, Appsequence 2117, Appsequence 2117, Appsequence 2115, Appsequence 2118, Appsequence 211
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Sequence 367, App
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Sequence 2001,
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Sequence 1089,
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APPLICANT: Wang, Ajun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEC ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1073, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lodes, Michael J.
Secrist, Heather
Benson, Darin R.
Meagher, Madeleine Joy
Stolk, John A.
Mang, Tongtong
Jiang, Yuqiu
Smith, Carole Lynn
King, Gordon E.
       11173
1200
1200
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     US-09-922-217-1073
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APPLICANT:
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-MODEL=frame+ p2n. model - DEV=xlp
-MODEL=frame+ p2n. model - DEV=xlp
-GG=y = 1/USPTO spool p/US09525041/runat_31122003_091151_11986/app_query.fasta_1.327
-GG=y = 1/USPTO spool p/US09525041/runat_31122003_091151_11986/app_query.fasta_1.327
-DB=bublished Applications NA -QFMT=fastap -SUFFXX=rnpb -WIRNATCH=0.1
-LOOPCL=0 - LOOPEXT=0 - UNITG=bits -START=1 - END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 - DOCALIGN=200 -THR SCORE=pct -THR MAX=10
-THR NIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXEN=200000000 -USER=US09525041 @CGN 1 1.107 @runat 31122003 091151_11986
-NCPU=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -WART -DSPBLOCK=100
-LONGLOG -DEV TINEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                            December 31, 2003, 10:05:14; Search time 2709 Seconds (without alignments) 201.876 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            78
MASRSMRLLLLLSCLAKTGV.....LTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCTNEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PCTNEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                               OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2263443 seqs, 1730637950 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                    0.5
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, Ygapext
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seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                    US-09-525-041-2
                                                                                                                                                                                                                                                                                                                                                                                                                 Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Pred. No.

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Score

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Percent Similarity:
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Sequence 1073, Application US/09833263

Sequence 1073, Application US/09833263

Sequence 1073, Application US/09833263

Sequence 1073, Application

GENERAL INFORMATION:

APPLICANT: Clapper, Jonathan D.

APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C12

CURRENT APPLICATION NUMBER: US/09/833.263

CURRENT FILING DATE: 2001.04-10

NUMBER OF SEQ ID NOS: 1093

CURRENT FILING DATE: 2001.04-10

SEQ ID NO 1073

LENGTH: 474

TYPE: DNA

TYPE: DNA

GRANISM: Homo sapiens

US-09-833-263-1073
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Matches:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-217-1073
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Best Local Similarity: 1
Query Match:
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Score:
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                    SEQ ID NO 1073
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APPLICANT: Xu, Jiangchun;
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Mang, Tongtong
APPLICANT: Wang, Yuqiu
APPLICANT: Wang, Yuqiu
APPLICANT: Wang, Yuqiu
APPLICANT: Wang, Yuqiu
APPLICANT: Wang, Alun
APPLICANT: Carper, Jonathan D.
APPLICANT: Capper, Jonathan D.
APPLICANT: Capper, Jonathan D.
APPLICANT: Carer, Darrick
APPLICANT: Sang IN NOW 1129
SURFARM FILLURG DARRE: 2001-12-19
SERQ ID NO 1073
SERQ ID NO 1073
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Conservative:
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                           Mismatches:
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US-10-025-380-1073
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     61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1075
LENGTH: 614
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Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Mang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wing, Yongtu
APPLICANT: Wing, Applicant
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CORGANISM: Homo sapiens
US-09-922-217-1075
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Conservative:
Mismatches:
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; Publication No. US20030104412A1
; GENERAL INFORMATION:
   APPLICANT: Heiskala, Marja
; TITLE OF INVENTION: REG-LIKE PROTEIN
   FILE REFERENCE: CDS-261
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/276,414
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO.
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ORGANISM: Human
Alignment Scores:
Pred. No.:
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US-10-100-608B-1
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MetalaSerArgSerMetargLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal 20 US-09-525-041-2 (1-158) x US-09-922-217-1075 (1-614)

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                                                                                               GluTyrIleSerGlyTyrGlnArgSerGlnProIleTrpIleGlyLeuHisAspProGln 100
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                       TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secriter, Heather
APPLICANT: Secriter, Heather
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Carper, Gary R.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
CURRENT FILING DATE: 210121.471C14
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTHARE: FastSEQ for Windows Version 4.0
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LENGTH: 614
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Sequence 1075, Application US/09833263

Patent No. US20020110547A1

GENERAL INFORMATION:

APPLICANT: Wang, Aijun

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Madelen J.

APPLICANT: Stolk, John A.

APPLICANT: Madelen J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 21012.1.471C12

CURRENT APPLICATION WUMBER: US/09/833,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1075

LENGTH: 614
                                                                                                                                        376 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACA 435
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                                     LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn
                                                                             CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT
                                                                                                              CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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ORGANISM: Homo sapiens
US-09-833-263-1075
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                                                                                                                                                                      351 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGAC
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                                                              61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                     411 AAGAGGCAGCAGTGGCAGTGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC
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CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1074
LENGTH: 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1074, Application US/0992217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Wu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Heather
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Sinth, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
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CRGANISM: Homo sapiens
US-09-922-217-1074
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                                                                                 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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  CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                        TGGAGCAGCAACGAATGCAACAAGGCCCAACAACATTCCTGTGCAAGTACCGACCA 609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Mang, Aljun
APPLICANT: Mang, Aljun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND COMPOUNDS
FILE REFERENCE: 210121.471C13
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARER FESTSEQ FOR Windows Version 4.0
SEQ ID NO 1071
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Wing, Tuqiu
APPLICANT: Sith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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ORGANISM: HOMO
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| Sequence 1071, Application US/09833263 |
| Sequence 1071, Application US/09833263 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: Wang, Aliun A. |
| APPLICANT: Stolk, John A. |
| APPLICANT: Stolk, John A. |
| APPLICANT: Clapper, Jonathan D. |
| APPLICANT: Madelein J. |
| TITLE OF INVENTION: COMPOUNDS FOR THEIR USE |
| TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE |
| FILE REFERENCE: 21011.471C12 |
| CURRENT FILING DATE: 2001.04-10 |
| NUMBER OF SEQ ID NOS: 1093 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 1071 |
| LENGTH: 1114
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; ORGANISM: Homo sapiens
US-09-833-263-1071
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Best Local Similarity:
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Sequence 1074, Application US/09833263

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Sequence 1074, Application US/09833263

GENERAL INFORMATION:

APPLICANT: Clapper, John A.

APPLICANT: Meagher, Madelein J.

APPLICANT: Meagher, Madelein J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471012

CURRENT APPLICATION NUMBER: US/09/833,263

CURRENT APPLICATION NUMBER: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOUTHANDR: FEASTERQ for Windows Version 3.0
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TrpSerSerAanGluCy8AanLy8ArgGlnHiaPheLeuCy8Ly8TyrArgPro 158
                                                                                                                    Sequence 1, Application US/09525041

Publication No. US20030158098A1

GENERAL INFORMATION:

TITLE OF INVENTION: Colon Specific Gene and Protein

FILE REFERENCE: PF178D2

CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: US/09/525,041

CURRENT FILING DATE: 2004-06-04

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-29

NUMBER: OF SEQ ID NOS: 6

SOFTWARE: PATCHING DATE: 1995-06-06

SEQ ID NO: 6

SEQ ID
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878.00
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; LOCATION: (111)..(587)
US-09-525-041-1
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US-10-025-380-1071
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APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
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Sequence 1071, Application US/10025380 Publication No. US20020182191A1 GENERAL INFORMATION:
                                                                 APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Macher: Macheline Joy
APPLICANT: Stolk, John A.
APPLICANT: Mang, Tongtong
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
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ORGANISM: Homo sapiens
US-10-025-380-1071
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CARTER, DAIRICK
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1114
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Matches:
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S-10-025-380-1074
Sequence 1074, Application US/10025380
Publication No. US20020182191A1
GENERAL INFORMATION:
                                                                       APPLICANT: XX. Jangchun
APPLICANT: XX. Jangchun
APPLICANT: Godes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, On A.
APPLICANT: Magher, Madeleine Joy
APPLICANT: Mang, Tongtong
APPLICANT: Mang, Tongtong
APPLICANT: Sinth, Carole L.
APPLICANT: Sinth, Carole L.
APPLICANT: King, Gordon B.
APPLICANT: King, AJun
APPLICANT: King, AJun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick Thomas S.
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CORGANISM: Homo sapiens
US-10-025-380-1074
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Best Local Similarity:
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US-10-157-031-113

Sequence 113, Application US/10157031

Sequence 113, Application No. US20030108890A1

Sequence 113, Application No. US20030108890A1

GENERAL INFORMATION:

APPLICANT: Baranova, A. V.

APPLICANT: Kozlov, A. V.

APPLICANT: Lobashev, A. V.

APPLICANT: Lobashev, A. V.

APPLICANT: Lobashev, A. V.

APPLICANT: Krukovakaya, L. L.

TILE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REFERENCE: 2760-103

CURRENT APPLICATION NUMBER: US/10/157,031

CURRENT FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 415

SOFTWARE: PatentIn version 3.1
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score greater than or equal to the score of the result being printed,
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version 5.1.6
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Human colon tumour

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121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
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                                                                                                                                                                                                                                                                                                                                                Human proteins with secretory signal sequences - used to treat immune deficiencies, infections, tumours, and haematopoietic
                              /*tag= a
/product= "human protein comprising secretory
signal"
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 Location/Qualifiers
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(SAGA ) SAGAMI CHEM RES CENTRE.
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AAGAGGCAGCAGTGGCAGTGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGG

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The present invention describes colon tumour associated proteins (I) and the present invention describes colon tumour associated protein. (I) and (II) and (II) and be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) carpersaion, such as colonic cancer. For example, (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the cused to treat disorders associated with decreased expression by activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to patients own production of them. Additionally, (II) may be used to conflict the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The and in a seape to identify modulators of TCAP expression and activity. The and in the presence of TCAPs in samples, and in assays to identify modulators of TCAP expression and activity. The and activity. The anti-(I) antibodies and anti-(I) antibodies may also be used as diagnostic and antadomism and activity. The and activity of and activity. The and activity of and activity are and anti-(II) antibodies and anti-(II) antibodies may also be used to down regulate (e.g. by enzyme linked immunosorbant assays (ELISA)). AAI28460 to AAI29512 and AAMX4494 to AAMX4523 represent invention.

Given in the exemplification of the present invention.
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141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
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                                                                                       Benson DR, Meagher MJ, Stolk JA;
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immunogenic; gene therapy; vaccine; colonic cancer; ss.
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15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-0609448.
28-AUG-2000; 2000US-0649811.
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                                                                                                                                     41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                              TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                      241 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG
                                                                                                                                                                                                                                                    MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                                                                                                                                                                                                      Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
      other;
                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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/*tag= a
/partial
/product= "TSA7005 protein"
/note= "no stop codon given"
     G; 103
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     129
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                        1.14e-86
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     126 A; 116
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    Sequence 474
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                 Alignment Scores:
Pred. No.:
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                                                                                                                                                                                        The present sequence encodes a human TSA7005 protein which shares 32% homology with human and mouse Reg proteins, and 34% homology with the rat Reg protein. TSA7005 has pancreatic beta cell growth activity and hypoglycaemic activity. The TSA7005 protein can be used for the diagnosis and treatment of diseases associated with the gene and its expression product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GAGTACATAAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSA7005 gene, encoding a polypeptide useful for the diagnosis and treatment of diseases associated with its expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon specific gene cDNA sequence SEQ ID NO:1073
                                                                                                                                                                                                                                                                                                                               C; 129 G; 103 T; 0 other;
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Matches:
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Mismatches:
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Gaps:
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(SAKA ) OTSUKA PHARM
                                    WPI; 2001-303742/32.
P-PSDB; AAB74934.
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Best Local Similarity:
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101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
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                                                                                                                                                                                                                    (first entry)
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Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer; tumour; immune response; immunostimulant; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                         New polynucleotide, useful for the preparation of a composition stimulating an immune response against, or treating, cancer
                                                                                                                                                                                                                    Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences used in the exemplification of the present invention
                                                                                                                                                                                                                  Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk
Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD;
Skeiky YAW, Fanger GR, Vedvick TS, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 474 BP; 126 A; 116 C; 129 G; 103 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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03-AUG-2001; 2001US-0922217.
19-DEC-2001; 2001US-0025380.
                                                                                                                     39-APR-2002; 2002WO-US11475
                                                                                                                                                                                                                                                                   WPI; 2003-067548/06.
                                                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                      WO200283070-A2.
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                                                Homo sapiens
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Pred. No.:
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                       gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting the presence of a tumor comprises detecting the concentration of a Reg Like Protein or the presence or quantity of a nucleic acid encoding it -
                                                                           121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr
361 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; REG-like protein; RELP; tumour; cancer; therapy; chromosome 1;
                                                                                                                                                                                      Seguence 477 BP; 127 A; 116 C; 130 G; 104 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human REG-like protein (RELP) cDNA.
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121 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT 180
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immunoglobulin; cytostatic; Ig agonist; immunoglobulin agonist; cancer;
protein therapy; RELP human Ig derived protein; chromosome 1p12-13.1;
                                                                                                                                                                                                                                                                      LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCACCACCATAGCA
                                                                                                                                                                       MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
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                                                                                                                                                                                                                         The present sequence encodes a new isolated REG-like protein (RELP) human immunoglobulin (Ig) derived protein. RELP comprises: (a) a human variable and constant region; or (b) an isolated human Ig derived protein or specified portion or variant encoded by a nucleic acid. RELP has cytostatic activity and can be used as an Ig agonist and in protein therapy. The RELP human Ig derived protein or a specified portion or variant can be used for preventing or treating a RELP protein mediated condition, malignant condition of disease condition, e.g. cancer. The nucleic acids can be used in producing RELP Ig derived protein. The human RELP protein of the present invention is located to
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                                                                                                                  New isolated REG-like protein (RELP) human immunoglobulin derived protein or specified portion or variant, useful for preventing or treating a RELP protein mediated condition or malignant condition,
                                                                                                                                                                                                                                                                                                                                                                                                                0 other;
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Matches:
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                                                                      61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Reg 1-gamma protein cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            AAI29510 standard; cDNA; 614
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15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
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29-JUN-2000; 2000US-0609448
28-AUG-2000; 2000US-0649811.
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                                                                                                                            regulation; cell growth; development; tumourogenesis; neurodegeneration;
inhibition; treatment; prevention; neoplasia; metastasis;
neurodegenerative change; Alzheimer's disease; Down's syndrome;
regeneration; pancreatic beta-cells; diabetes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human Reg I-gamma protein, which comprises a C-type lectin. The sequence was identified in Incyte clone 1310334. Reg I-gamma protein is involved in regulation of call growth and development. Since the overexpression of reg proteins is associated with tumourogenesis and neurodegeneration, inhibition of human Reg I-gamma expression can be used for treading or preventing neoplasia or metastasis and neurodegenerative changes associated with Alzheimer's disease and other disorders of the central nervous system, e.g. Down's syndrome. Reg I-gamma can also be used in therapeutics to induce regeneration of pancreatic beta-cells in the treatment of disabetes. The products can also be used for detection for, e.g. expression of REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human Reg I-gamma protein - useful for developing products for treating, e.g. diabetes, tumours or neuro-degenerative disease such as Alzheimer's
                                                                                                                Human; Reg I-gamma protein; C-type lectin; Incyte clone 1310334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 614 BP; 168 A; 143 C; 171 G; 132 T; 0 other;
                                                                                    cDNA encoding a human Reg I-gamma protein.
                                                                                                                                                                                                                              Location/Qualifiers
136..612
/*tag= a
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HP.
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614
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                                                       (first entry)
AAV29156 standard; cDNA;
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(first entry)

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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by
                                                                            JA;
                                                                                                                                                                                                                                                                         Colon tumor associated proteins and nucleic acids useful for prevention, diagnosis and treatment of colonic cancer -
                                                                                Meagher MJ,
                                                                            Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 465; 472pp; English
                                                                        Secrist H,
Jiang Y;
CORI-) CORIXA CORP
                                                                                                                                                                                        WPI; 2001-441847/47.
                                                                            Xu J, Lodes MJ,
King GE, Wang T,
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US-09-525-041-2 (1-158) x AAV29156 (1-614)

614 158 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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Percent Similarity: Best Local Similarity:

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Alignment Scores:

LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40

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CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTACCACAAGTCCAAT

255

99US-0476296

tumour; immune response; immunostimulant; cytostatic; vaccine

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rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host call culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (FCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigons in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples. (G.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAVA14944 to AAVA1523 represent nucleotide and amino acid sequences
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Sequence 614 BP; 168 A; 143 C; 171 G; 132 T; 0 other;

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ò	н	MetAlaSerArg	CArgSerMetArgLeuLeuLeuL	uLeuLeuLeuLeuSerC	CysLeuAlaLysThrGlyVal	(4
q	136		AGAAGCATGCGGCT	GCTCCTATTGCTGAGC	HILLINITITITITITITITITITITITITITITITITITI	П
ò	21		ollelleMetArgPr	LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHi	TrpPheTyrHisLysSerAsn	4
q	196		TATCATCATGAGACC	CAGCTGTGCTCCTGGA	CTGGGTGATATCATCATCAGGTGCTCTGCTCCTGGATGGTTTTACCACAAGTCCAAT	r.d
ò	41	-	TyrPheArgLysLe	WArgAsnTrpSerAsp	CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer	Ψ
q	256	-	TACTTCAGGAAGCT	GAGGAACTGGTCTGAT	TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT	(,,
ò	61	-	GlyalaHisLeuAl	aSerlleLeuSerLeu	TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla	w
q	316		GGAGCCCACCTGGC	ATCTATCCTGAGTTTA		m
ò	. 81		SerGlyTyrGlnAr	gSerGlnProlleTrp	GluTyrIleSerGlyTyrGlnArgSerGlnProlleTrpIleGlyLeuHisAspProGln	
q	376		AGTGGCTATCAGAG			4
ઠે	101		GlnTrpGlnTrpI	eAspGlyAlaMetTyr	LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly	_
q	436		SCAGTGGCAGTGGAT	TGATGGGGCCATGTAT	AAGAGGCAGCAGTGGCATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC	4
ò	121	LyBS	GlyGlyAsnLysHi	SCysAlaGluMetSer	erMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr	_
q	496	-	GGTGGGAACAAGCA	CTGTGCTGAGATGAGC	AGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT	L)
È	141	_	TrpSerSerAsnGluCysAsnLy	8AsnLysArgGlnHisPheLeu(CystysTyrArgPro 158	
g	556	-	CAACGAATGCAACAA	TGGAGCAGCAACGAATGCAACAAGCGCCAACACTTCCTGTGCAAGTACCGACCA	TGCAAGTACCGACCA 609	
RESULT ABZ3369 ID AB	лт 9 13696 ABZ33696	standard	; CDNA; 614 BP.			
X 2 :	ABZ33696					
žĖ:	30-JAN-2	2003 (first	st entry)			
名	Human co	colon specific	gene cDNA	sequence SEQ ID N	NO:1075.	
X	Human; co	colon cancer;	ir; colon tumour;	r; immunotherapy;	; diagnosis; cancer;	
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The present invention describes compounds (I) for the immunotherapy and diagnosis of colon cancer. Also described: (1) a method for detecting the presence of cancer in a patient; (2) a method for stimulating and/or expanding T cells specific for a tumour protesh; (3) an isolated T cell population comprising T cells prepared by the method of (2); (4) a method for stimulating an immune response in a patient; (5) a method for treating cancer in a patient; and (6) a method for inhibiting the development of cancer in a patient. (1) have immunostimulant and cytostatic activities and can be used in vaccines ABZ12646 to ABZ13725 and ABP55143 represent human colon cancer/tumour related sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACATAGCA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 ATGGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCTGGCCAAAACAGGAGTC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 CTGGGTGATATCATCATGAGACCCCAGCTGTGCTCCTGGATGGTTTTTACCACAGTCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer
                                                                                                                                                                                                                                                                                                  Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA; Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD; Skeiky YAW, Fanger GR, Vedvick TS, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 614 BP; 168 A; 143 C; 171 G; 132 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 467; 537pp; English.
                                                                                                                                                                                        10-APR-2001; 2001US-0833263.
03-AUG-2001; 2001US-0922217.
19-DEC-2001; 2001US-0025380.
                                                                                                                                                       09-APR-2002; 2002WO-US11475.
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Query Match:
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Percent Similarity:
                                                   Homo sapiens.
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                    gene; ss.
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127 CTGGGTGATATCATCATGAGACCCAGCTGTGCTCCTGGATGGTTTTACCACAAGTCCAAT 186
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/note= "5' primer site for PCR amplification
and baculovirus expression"
complement (112..128)
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gene therapy; ss.
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111..587
4.tag= a
/product= mature colon specific protein
complement (111..130)
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/note= "5'
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P-PSDB; AAW12691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a human TSA7005 protein which shares 32% homology with human and mouse Reg proteins, and 34% homology with the rat Reg protein. TSA7005 has pancreatic beta cell growth activity and hypoglycaemic activity. The TSA7005 protein can be used for the diagnosis and treatment of diseases associated with the gene and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
                                                                                                                  141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                       TGGAGCAGCAACGAACAACAACACACTTCCTGTGCAAGTACCGACCA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSA7005 gene, encoding a polypeptide useful for the diagnosis and treatment of diseases associated with its expression -
                                                                                                                                                                                                                                                                                                                                                      TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 269 A; 278 C; 247 G; 264 T; 2 other;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                         Human TSA7005 protein encoding cDNA SEQ ID NO:3.
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/product= "TSA7005 protein"
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67..543
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P-PSDB; AAB74934.
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Pred. No.:
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Query Match:

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viability; colon cancer cell;

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                                                                                            A cDNA clone (AAT51784) codes for a colon specific protein (AAW12691) that may be useful as a diagnostic marker for colon cancer. It is believed that the presence of active transcription of the colon specific gene in non-colon cells of a host is indicative of colon cancer metasteses. The cDNA, deposited as ATCC 97129, was isolated from a human colon cancer cDNA library. It can be used to design diagnostic probes, to produce recombinant colon specific protein in transformed host cells, in the gene therapy of patients having need of a colon specific gene protein, or to design antisense constructs useful for treatment of colon cancer.
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                in
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             colon specific gene - used to develop prods. for and treatment of colon disorders, partic. colon
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                                                                    Claim 4; Page 51-52; 64pp; English
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The present sequence represents a human colon specific gene. The nucleic acid sequence can be used to develop products for the diagnosis of a disorder of the colon, e.g. colon cancer or metastases. The products can also be used to screen for agonists or antagonists for the polypeptides. The antagonists may be used to treat colon cancer, since they interact with the function of colon specific polypeptides to inhibit functions which are necessary for the viability of colon cancer cells. The products can also be used for the production of antibodies and for the identification of receptors for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluTyr1leSerGlyTyrGlnArgSerGlnProlleTrp1leGlyLeuHisAspProGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human colon specific gene - used to develop products for the diagnosis and treatment of disorders of the colon, e.g. colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                /*tag= a
/note= "colon specific gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-525-041-2 (1-158) x AAX03195 (1-1114)
                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Fig 1A-C; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.56e-86
878.00
100.00%
100.00%
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                                                                                                                                                                                                                                                              Dillon PJ, Li Y, Soppet
                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                                                                                                                                               cancer and metastases
                                                                                                                                                                                                                                                                                          WPI; 1999-130432/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                        P-PSDB; AAW84274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                            Homo sapiens
                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                          06-JUN-1995;
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                                                                                                                                                    19-JAN-1999
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MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xu J, Lodes MJ,
King GE, Wang T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human colon specific polypeptides and polynucleotides for diagnosis and treatment of colon cancer, for screening compounds which interact with polypeptide, for synthesis of DNA and manufacture of DNA
LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
            LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr
                                                      AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT
                                                                                                                                                                                                                                         colon specific; colon cancer; metastasis; diagnose; treatment;
                                                                                    T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1114
158
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/product= "Colon specific protein"
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                    Human colon specific protein cDNA sequence
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                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 20pp; English
                                                                                                                                                    AAA62951 standard; cDNA; 1114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1114 BP; 288 A; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
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878.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-464055/40.
P-PSDB; AAB12900.
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                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1998;
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                                                                                                                                                                                                                                                      cytostatic;
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US-09-525-041-2 (1-158) x AAA62951 (1-1114)

Similarity:

Query Match: DB: Best Local

Percent Similarity:

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291. TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAAGGAAGCCAGCACCATAGCA 350
                                                          230
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                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                   470
                                                                                                                                                                                                                                                                                                                                  121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
                                                                                                                                                                                                                                                                                                                                                              530
                                                                                                                    231 IGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT 290
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                                                                                                                                                                                                                                                                         LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly
111 ATGGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCTGGCCAAAACAGGAGTC
                                                                                                                                                                                                              21 LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn
                                                                                          41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                   TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLygGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                        471 AAGTCCATGGGGAGCAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT
                                                                                                                                                                                                                                                                                                                                                                                          141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
                                                                                                                                                                                                                                                                                                                                                                                                             531 IGGAGCAGCAACGAATGCAACAAGAGCGCCAACATTCCTGTGCAAGTACCGACCA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon specific gene cDNA sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 464; 472pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI29506 standard; cDNA; 1114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1999; 99US-0476296.
10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0575251.
29-JUN-2000; 2000US-069448.
28-AUG-2000; 2000US-0649811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-441847/47
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The present invention describes colon tumour associated proteins (I) and the present invention describes colon tumour associated protein. (I) and (II) and (II) tan be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as Colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the cativity of TCAPs by expressing inactive proteins or complement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and character the presence of similar nucleic acids is samples, and the preduction and the production of antibodies against TCAPs also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies may also be used to as a diagnostic agents for detecting the presence of TCAPs in samples.

TCAP expression and activity. The anti-(I) antibodies may also be used to as diagnostic agents for detecting the presence of TCAPs in samples conditions against TCAPs and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
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Seguence 1114 BP; 288 A; 291 C; 262 G; 273 T; 0 other;

3	פלתבווכם	130 5111	200 A; 231 C;	202 6; 2/3 1; 0 7	סרוופד ;	
Alignment Pred. No.:		Scores:	3.56e-86		1114	
Score:			878.00		158	
Percent Sin	Simil	Similarity:	100.00%	Conservative:	00	
Query Match: DB:	atch:		100.00 \$ 22		>00	
US-09-525-041	25-041	2 (1-158)	x AAI29506	(1-1114)		
È	1	MetAl	CArgSerMetArgLe	aSerArgSerMetArgLeuLeuLeuLeuLeuSerCy	CysLeuAlaLysThrGlyVal 20	_
q	111		AGAAGCATGCGGCT	GCTCCTATTGCTGAGC		6
ò	21	LeuGl	YASDI]eI]eMetArgPr	eMetArgProSerCysAlaProGly	YTrpPheTyrHisLysSerAsn 40	_
ପ୍ପ	171	-				0
ò	41	_	TyrPheArgLysLe	uArgAsnTrpSerAspA	CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer 60	_
qq	231	-	FTACTTCAGGAAGCT	GAGGAACTGGTCTGATC		0
È	61	Tyrel	yAsnGlyAlaHisLeuAl	aSerIl	eLeuSerLeuLysGluAlaSerThrileAla 80	_
QQ	291	-	GGAGCCCACCTGGC	ATCTATCCTGAGTTTA	TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA 350	0
ò	81	-	SerGlyTyrGlnAr	gSerGlnProlleTrp	GluTyrIleSerGlyTyrGlnArgSerGlnProIleTrpIleGlyLeuHisAspProGln 100	0
ф	351	-	AGTGGCTATCAGAG	AAGCCAGCCGATATGG	GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG 410	0
È	101		GlnTrpGlnTrpIl	eAspGlyAlaMetTyrI	LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120	0
qq	411		SCAGTGGCAGTGGAT	TGATGGGGCCATGTATC	AAGAGGCAGCAGCAGCAGCAGTGGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC 470	2
ò	121		GlyGlyAsnLysHi	BCyBAlaGluMetSerS	LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140	9
QQ	471	-	GGTGGGAACAAGCA	CTGTGCTGAGATGAGC	AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAACTTTTTAACT 530	0
ò	141		CAShGluCysAshLy	TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro	CysLysTyrArgPro 158	
a	531		PACGAATGCAACAA	TGGAGCAGCAACGAATGCAACAAGCGCCAACACTTCCTGTGCAAGTACCGACCA		

Percent Similarity: Best Local Similarity:

Query Match: DB:

AAI29509 standard; cDNA; 1114 BP.

RESULT 15 AAI29509 ID AAI293

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Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                          Benson DR, Meagher MJ, Stolk JA;
                                                  Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic; gene therapy; vaccine; colonic cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1114 BP; 288 A; 291 C; 262 G; 273 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                   Human colon specific gene cDNA sequence #2.
                                                                                                                                                                                                                                                                     Claim 2; Page 465; 472pp; English.
                                                                                                                                30-DEC-1999; 99US-0476296.
10-JAN-2000; 2000US-0480321.
15-FEB-2000; 2000US-0504629.
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-057251.
29-JUN-2000; 2000US-069481.
28-AUG-2000; 2000US-0649811.
                                                                                                                                                                                                          Xu J, Lodes MJ, Secrist H,
King GE, Wang T, Jiang Y;
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878.00
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                                                                                                                  29-DEC-2000; 2000WO-US35596
                    (first entry)
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                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                     WO200149716-A2
                                                                        Homo sapiens.
                    12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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       AA129509;
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US-0;	US-09-525-041-2	-2 (1-158) x AAI29509 (1-1114)
ò	Ħ	MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal 20
qa	111	ATGGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCTGGCCAAAACAGGGGTC 170
ò	. 21	LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40
qq	171	CTGGGTGATATCATCATGAGACCCAGCTGTGTTCTTTACCACAAGTCCAAT 230
ò	41	CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer 60
q a	231	TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT 290
ò	61	TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla 80
qq	291	TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA 350
δ	81	GluTyrIleSerGlyTyrGlnArgSerGlnProIleTrpIleGlyLeuHisAspProGln 100
qq	351	GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACA 410
ò	101	LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
qa	411	AAGAGCAGCAGCAGTGGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC 470
ò	121	LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
qa	471	AAGTCCATGGGTGGGAACAAGCACTGTGTGTGTGTGTGTG
ò	141	TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
q	531	TGGAGCAGCAACGAATGCAACAAGGGCCAACACTTCCTGTGCAAGTACCGACCA 584

Search completed: December 31, 2003, 09:29:07 Job time : 254 secs

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BC017089 Homo sapt
BD167401 Method of
AF254415 Homo sapt
AF25430398 Sequence
AX351470 Sequence
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AX368758 Sequence
AX368758 Sequence
BC19465 Mus muscu
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BD062766 Human pro
ES141 TSA7005 gen
AX577651 Sequence
AX058965 Sequence
AX193508 Sequence
ES142 TSA7065 gen
AR030953 Sequence
AX100599 Sequence
AX193504 Sequence
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BD062775 Human pro
AX193502 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                           Description
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AX351280 S
AX340842 S
AX192921 S
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AX340869 S
AX341040 S
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AX261862
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AX335380
AX351470
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AX588758
BD108868
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AX379115
AX379125
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em_htgo_mus: *
em_htgo_other: *
                 em_htg_hum: *
em_htg_inv: *
em_htg_other: *
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em_htg_rod: *
em_htg_mam: *
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=sext -HEAPSIZE=500 -MINLEN=0 -NAXLEN=2000000000
-USRS=USO9525041 @CGN 1 1 4959 @runat 31122003 091149 11864 -NCPU=6 -ICPU=3
-NO WMAR -LARGEOUERY -NEG SCORES=0 -WAIT -NSPBLCOK=100 -LONGLOG
-NO WMAR -LARGEOUERY -NEG SCORES=0 -WAIT -NSPBLCOK=100 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                         December 31, 2003, 09:16:53 ; Search time 2146 Seconds (without alignments) 3011.986 Million cell updates/sec
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1 MASRSMRLLLLLGCLAKTGV......LTWSSNECNKRQHFLCKYRP 158
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                      nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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GI:22608369
                                       Homo sapiens
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Human proteins having secretory signal sequences and DNAs encoding
these proteins.
              PAT 15-AUG-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Compounds for immunotherapy and diagnosis of colon cancer and methods for their use
Patent: WO 0149916-A 1073 12-JUL-2001;
CORIXA CORPORATION (US)
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               linear
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Matches:
Conservative:
Mismatches:
Indels:
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         474 bp Di
Sequence 1073 from Patent W00149716.
AX193506
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a 116 c 129 g 103
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                                                  AX193506.1 GI:15211446
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878.00
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                                                                           Homo sapiens (human)
                                                                                         Homo sapiens
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Best Local Similarity:
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Xu,J.
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BD062766
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I. (bases I to 47). Kimura, T. and Kobayashi, M. Human proteins having secretory signal sequences and DNAs encoding
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SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
SAGAMI CHEMICAL RESEARCH
SP 2001506484-A/3
PN JP 2001506484-A/3
PP 12-SEP-1997 JP 1998513509
PR 13-SEP-1996 JP 8/243060
PI SEISHI KATO, SHINGO SEKINE, TOMOKO KIMURA, MIDORI KOBAYASHI PC
C12N15/12, C07K14/47, C12N15/62
CC Strandedness: Double;
CC Topology: Linear;
FH Key
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158
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Mismatches:
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878.00
100.00%
100.00%
JP 2001506484-A/3.
Homo sapiens (human)
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RESULT 3

ACCESSION

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PAT 23-NOV-2002
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     Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Butel
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo
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Sequence 1 from Patent EP1241269
AX537651 GI:25269611
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1. .474
/organism='Unknown'.
Location/Qualifiers
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Ogawara,T., Suzuki,M. and Ozaki,K.
TSA7005 gene
Patent: JP 2001025389-A 1 30-JAN-2001;
OTSUKA PHARMACEUT CO LTD
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/organism="unidentified"
/or_type="genomic DNA"
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a l16 c 129 g 103
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E52141.1 GI:18629624
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PAT 31-JAN-2002
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Stolk, J.A., King, G.E., Wang, T. and Jiang, Y.
Compounds for immunotherapy and diagnosis of colon cancer and
methods for their use
Patent: WO 0149716-A 1075 12-JUL-2001;
CORIXA CORPORATION (US)
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ORS Ogawara, T., Suzuki, M. and Ozaki, K.
TSA7005 gene
AL Patent: JP 2001025389-A 2 30-JAN-2001;
OTSUKA PHARNACEUT CO LTD
PN JP 2001025300
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TSA7005 gene.
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E52142.1 GI:18629625
JP 2001025389-A/2.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequence 1075 from Patent W00149716.
AX193508.1 GI:15211448
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Bandman,O. and Goli,S.K.
Human Reg protein
Patent: US 5837841-A 2 17-NOV-1998;
Location/Qualifiers
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Sequence 2 from patent US 5837841.
AR058965
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PF 15-JUL-1999 JP 1999201279
PR
PI TSUYOSHI OGAWARA,MIKIO SUZUKI,KOICHI OZAKI
PC C12N15/09,COTK14/47,C12N1/15,C12N1/19,C12N1/21, PC
C12N5/10//A61K31/00,
PC A61K38/00,A61K48/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 29-SEP-1999
                                                                                                                                                                                                                                                                                                                       ATGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCTGGCCAAAAAACAGGAGTC 126
                                                                                                                                                                                                                                                                                                                                                    246
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla 80
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                                                                                                                                                            2 others
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                                                                     Location/Qualifiers
(67)..(540).
Location/Qualifiers
1..1060
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
a 278 c 247 q 2641
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1 (bases 1 to 1114)
Soppet,D.N., Li,Y. and Dillon,P.J.
Colon specific gene and protein
Patent: US S861494-A 1 19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR030953 1114 bp
Sequence 1 from patent US 5861494.
AR030953
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best Local Simila Query Match: DB:	Sımılarıty: h:	100.00% 100.00% 6	Mismatche Indels: Gaps:	0	000		
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 ò	1 MetAlaSer	MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyval	Sulfeuleul	euLeuSer(Systemalar	ysThrGlyVal 20	
 _연	111 Argerre	CAGAAGCATGCGGCT	recreative	TGCTGAGC	recereecea	AAACAGGAGTC 170	_
 ò	21 LeuGlyAsp	LeuGlyAspIleIleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn	COSerCysA	laProGly	rpPheTyrH	isLysSerAsn 40	
 셤	171 creecrear	ratcarcardadacc	caccicio	crecredar	regritiaco	ACAAGTCCAAT 230	_
 ò		CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer	ewArgAsnT	rpSerAsp/	AlaGluLeuG		
d G	231 TGCTATGGI	rtacttcaggaagc1	rgaggaact.	GGTCTGAT(SCCGAGCTCG	AGTGTCAGTCT 290	_
 ò		TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLygGluAlaSerThrIleAla	aSerIleL	euSerLeul	ysGluAlaS	æ	
92	291 TACGGAAAC	desacceaceres	arcrarcc	rcacrtra	vaggaagcca	ĠĊĄĊĊĄTĄĠĊĄ 350	_
ò	81	GluTyrIleSerGlyTyrGlnArgSerGlnProlleTrplleGlyLeuHisAspProGln	GSerGlnP	rolleTrp	leGlyLeuH:		_
qq	351 GAGTACATA	AGTGGCTATCAGAC	PAGCCAGC	cgarargg	vrreecerec		_
 ò		LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly	eAspGlyA	laMetTyr1	euTyrArgSe	erTrpSerGly 120	_
 QQ Q	411 AAGAGGCAG	scadrodcadroda	TĠATĠĠĠ	ccarctar	retacagar	ccrearcrace 470	_
č	121 LysSerMet	LysSerWetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr	SCYBALAG	luMetSer	serAsnAsnA	snPheLeuThr 140	_
 qq	471 AAGTCCATG	SGGTGGGAACAAGCA	crerecte.	AGATGAGC	CCAATAACA	ACTITITAACT 530	
 ò	141 TrpSerSer	TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro	'sArgGlnH.	isPheLeu(YBLYBTYEA	rgPro 158	
qa	531 TGGAGCAGC	CAACGAATGCAACAA	GCGCCAAC	Actricing	GCAAGTACC	GACCA 584	
 RESULT 9 AR100599 LOCUS DEFINITION ACCESSION VERSION KEYMODIS	AR100599 Sequence 1 AR100599 AR100599.1	1: from patent US GI:12811047	.114 bp ; 6080722	DNA .	linear	PAT 14-FEB-2001	-
 တ	Unknown. Unknown.	3					
 REFERENCE AUTHORS TITLE	Oncidebille 1 (bases 1 Soppet, D.R. Colon speci	Unclassified. 1 (bases 1 to 1114) Soppet, D.R., Li.Y. and Dillon, P.J. Colon specific gene and protein	llon, P.J. grotein				
 JOURNAL FEATURES	Patent: US Lo	6080722-A 1 27 ocation/Qualifi 1114	-JUN-200(.; 0			
 BASE COUNT ORIGIN	288 a	organism="unknown" 291 c 262 g	wn" 9 27.	ω τ			
lignment red. No.:	Scores:	9.01e-83	Length:		1114		
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Oy 1 MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal 20	Qy 21 LeuGlyAspileileMetargProSerCysalaProGlyTrpPheTyrHisLysSerAsn 40	Qy 41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer 60		GluTyrIleSerGlyTyrGlnArgSerGlnProIleTrpIleGlyLeuHisAppProGln 	101 LysargdlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly	121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnPheL 	Oy 141 TrpSerSerAanGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158 	RESULT 11 AX193507 LOCUS LOCUS AX193507 LOCUS DEFINITION Sequence 1074 from Patent W00149716.		_	CB 1 RS Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.A., King,G.E., Wang,T. and Jiang,Y.	TITLE Compounds for immunotherapy and diagnosis of colon cancer and methods for their use of the colon cancer and compounds to the colon cancer and ca	_ 0	/organism="Homo sapiens" //organism="Homo sapiens" //ol_type="genomic_DNA"	ADSE COUNT 288 a 291 c 262 g 273 t ORIGIN	scores: 9.01e-83 Length:	ilarity: 100. Similarity: 100.	100.00% Indens:	US-09-525-041-2 (1-158) x AX193507 (1-1114) Qy	Db 111 ATGGCTTCCAGAAGCATGCGGCTGCTCCTATTGCTGAGCTGCCTGGCCAAAACAGGAGTC 170 Ov 21 LeuGlyAspile1leMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40	
Match: 100.00%	-09-525-041-2 (1-158) x AR100599 (1-1114) 1 MetAlaSerArgSerMetArgLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal 20	Db 111 ATGGCTTCCAGAAGCATGCGGCTGCTCTATTGCTGGCCTGGCCAGAACAGGAGTC 170 Qy 21 LeuGlyAspilelleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40	41 CysTyrGlyTyrPheArgLysLeukrgAsnTrpSerAspAlaGluLeuGluCysGlnSer 	TyrGlyAanGlyAlaHisLeuAaSerIleLeuSerLeuLysGluAlaSerThrIleAla 	ProGln CACAG	Oy 101 LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120	Qy 121 LysSerMetGlyGlyAsnLysHisCysAlaGluMetSerSerAsnAsnAsnPheLeuThr 140	Oy 141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158	T 10 504	LOCUS AX193504 1114 bp DNA linear PAT 15-AUG-2001 ACTESSION AX193504 VERSION AX193504.1 GI:15211444		Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS Xu,J., Lodes,M.J., Secrist,H., Benson,D.R., Meagher,M.J., Stolk,J.A., King,G.E., Wang,T. and Jiang,Y. TITUE Commonings for imminotherany and diagnosis of colon cancer and	methods for their use AL Patent: W0 0149716.7 12-JUL-2001;	COKIMA CORPORATION (US) FEATURES Location/Qualifiers Source 1 .1114	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:966"	BASE COUNT 288 a _ 291 c 262 g 273 t ORIGIN	9.01e-83 Length: 878.00 Matches:	Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps:	525-041-2 (1-158) x AX193504 (1-1114)	

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AXUU/243 1130 bp mRNA linear PRI 23-APR-2001
Homo sapiens regenerating gene type IV mRNA, complete cds.
AX007243
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Hartupes, J.C., Zhang, H., Bonaldo, M.F., Soares, M.B. and
Dieckgraefe, B.K.
Isolation and characterization of a cDNA encoding a novel member of
the human regenerating procein family: Reg IV
Biochim. Biophys. Acta 1518 (3), 287-293 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (18-AUG-2000) Gastroenterology, Washington University
School of Medicine, 660 S. Euclid Ave., Campus Box 8124, St. Louis,
MO 63110, USA
LysSerMetGlyGlyAgnLysHisCysAlaGluMetSerSerAgnAgnAgnPheLeuThr
                                                                                                                                                                       483 AAGTCCATGGGTGGGAACAAGCACTGTGTGTTTTTAACT
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Dieckgraefe, B.K., Hartupee, J.C., Zhang, H., Soares, M.B. and
Bonaldo, M.F.
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1. 1130
(organism="Homo sapiens"
mol_type="mRNA"
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                                                                                                                              GluTyrileSerGlyTyrGlnArgSerGlnProileTrpileGlyLeuHisAspProGln 100
                                                                                                                                             351 GAGTACATAAGTGGCTATCAGAGAAGCCAGCCGATATGGATTGGCCTGCACGACCCACAG 410
                                                                                                                                                                                LysArgGlnGlnTrpGlnTrpIleAspGlyAlaMetTyrLeuTyrArgSerTrpSerGly 120
                                                                                                                                                                                                          411 AAGAGGCAGTGGCAGTGGATTGATGGGGCCATGTATCTGTACAGATCCTGGTCTGGC 470
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baranova,A.V., Yankovsky,N.K., Kozlov,A.P., Lobashev,A.V. and Krukovskaya,L.L.
In silico screening for phenotype-associated expressed sequences Patent: WO 02103028-A 113 27-DEC-2002;
Biomedical Center (RU)
Location/Qualifiers
1. .1130
                                                                          61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                       CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                       231 TGCTATGGTTACTTCAGGAAGCTGAGGAACTGGTCTGATGCCGAGCTCGAGTGTCAGTCT
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Sequence 113 from Patent WO02103028.
AX676920
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
a 293 c 265 g 28:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1E 1 (bases 1 to 1152)

1S Kato, S. Sekine, S., Kimura, T. and Kobayashi, M.

Human proteins having secretory signal sequences and DNAs encoding these proteins

1D Patent: JP 2001506484-A 12 22-MAY-2001;

SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

OS Homo sapiens (human)

PP 12-SEP-1997 JP 1998513509

PR 13-SEP-1997 JP 1998
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                                                                                                                                                                                                                                                    327 TACGGAAACGGAGCCCACCTGGCATCTATCCTGAGTTTAAAGGAAGCCAGCACCATAGCA 386
                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                   41 CysTyrGlyTyrPheArgLysLeuArgAsnTrpSerAspAlaGluLeuGluCysGlnSer
                                                                                                                                                                                                       61 TyrGlyAsnGlyAlaHisLeuAlaSerIleLeuSerLeuLysGluAlaSerThrIleAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507 AAGTCCATGGGTGGGAACAAGCACTGTGCTGAGATGAGCTCCAATAACAATTTTAACT
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/organism="Homo sapiens"
/nol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                             1 MetalaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLygThrGlyVal
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Stolk,J.A., King,G.B., Wang,T. and Jiang,Y.
Compounds for immuntherapy and diagnosis of colon cancer and methods for their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 TrpSerSerAsnGluCysAsnLysArgGlnHisPheLeuCysLysTyrArgPro 158
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Sequence 1072 from Patent WO0149716.
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/organism="Homo sapiens"
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298 c 275 g 28
US-09-525-041-2 (1-158) x AY007243 (1-1130).
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                                                          21 LeuGlyAspilelleMetArgProSerCysAlaProGlyTrpPheTyrHisLysSerAsn 40
            1 MetAlaSerArgSerMetArgLeuLeuLeuLeuLeuSerCysLeuAlaLysThrGlyVal 20
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APPLICANT: Lodes, Micheel J.
APPLICANT: Secrist, Heather
APPLICANT: Becrist, Heather
APPLICANT: Becrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, John A.
APPLICANT: Wang, Yugiu
APPLICANT: Wing, Carole Lynn
APPLICANT: Ming, Yugiu
APPLICANT: Ming, Gordon E.
APPLICANT: Ming, Ajun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND STRICK USE
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND STRICK USE
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND METHODS FOR THEIR USE
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE REPRESENCE: 2001-04-03
NUMBER OF SEQ ID NOS: 1124
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US-09-999-832A-452
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Patent No. US20020076414A1
GENERAL INFORMATION:
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Sequence 1077, A
Sequence 1078, A
                                                                                                                                                                                                            December 31, 2003, 09:15:03 ; Search time 72 Seconds (without alignments) 440.296 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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APPLICANT: Maith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Gapper, Jonathan D.
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
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Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 158; Conservative 0; Mismatches 0;
                                                                                                                                      NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                               CURRENT APPLICATION NUMBER: US/09/922,217 CURRENT FILING DATE: 2001-08-03
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Patent No. US20020076414A1
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APPLICANT: Lodes Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Maegher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Mangy Tongtong
                       TITLE OF INVENTION: OF COLORS FILE REFERENCE: 210121.471C13
                                                                                                                                                                                                                                                   TYPE: PRT
GRGANISM: Homo sapiens
US-09-922-217-1078
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US-09-922-217-1079
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                                                                                                                                                                                              SEQ ID NO 1078
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.471013
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1077
TENGIN: 158
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Sequence 1078, Application US/09922217
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heacher
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Smith, John A.
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonathan D.
                                                                                                                                                                                                                                                                                                              Sequence 1077, Application US/09922217
Patent No. US20020076414A1
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Secrist, Heather
Benson, Darin R.
Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yudiu
Smith, Carole Lynn
King, Gordon E.
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APPLICANT: Xu, Jiangchun
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US-09-922-217-1077
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Query Match
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US-09-833-263-1070

Sequence 1070, Application US/09833263

Batent No. US20020110547A1

GENERAL INFORMATION:
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Madeller, Madeller, Madeller D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REPREMENCE: 21012.1.4716.12

CURRENT APPLICATION NUMBER: US/09/833,263

CURRENT FILING DATE: 2001-04-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FESTERE OF TWINDOWS VERSION 3.0

SEQ ID NO 1070

LENGTH: 158
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
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100.0%; Score 878; DB 9;
Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 158; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                     RESULT 5
US-09-922-217-1080
; Sequence 1080, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Measher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Mang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                      Jiang, Yuqiu
Smith, Carole Lynn
King, Gordon E.
Wang, Aijun
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ORGANISM: Homo sapiens
US-09-833-263-1070
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Best Local Similarity
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APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE BEPERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1078
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      Length 158;
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Query Match 100.0%; Score 878; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 158; Conservative 0; Mismatches 0;
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Patent No. US20020110547A1
GENERAL INFORMATION:
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; Patent No. US20020110547A1
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CORGANISM: Homo sapiens
US-09-833-263-1077
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RESULT 12
US-10-295-027-138
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CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1079
LENGTH: 158
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; Sequence 1080, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: CLAPPENCE: 210121.471C12
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Best Local Similarity 100.0%; Pred. No. 7.6e-86;
Matches 158; Conservative 0; Mismatches 0; Indels 0
                                                                                                      Length 158;
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; Pred. No. 7.6e-86;
0; Mismatches 0;
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Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 158; Conservative 0
               TYPE: PRT; ORGANISM: Homo sapiens
US-09-833-263-1078
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US-09-833-263-1079
LENGTH: 158
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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Publication No. US20030158098A1
GENERAL INFORMATION:
TITLE OF INVENTION: Colon Specific Gene and Protein
FILE REPERENCE: PF178D2
CURRENT APPLICATION NUMBER: US/09/525,041
CURRENT FILING DATE: 1908-09-29
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
NUMBER PATENTIN VERSION 3.0
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CURRENT APPLICATION NUMBER: US/09/833,263
UNRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PASTSEQ for Windows Version 3.0
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
                                                                                                                                                                                              ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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CURRENT APPLICATION NUMBER: US/10/295,027

CURRENT FILING DATE: 2002-11-13

FRIOR PELICATION NUMBER: US 60/350,666

FRIOR PELING DATE: 2000-11-13

FRIOR PELING DATE: 2001-11-13

FRIOR PELING DATE: 2001-11-15

FRIOR PELING DATE: 2001-11-15

FRIOR PELING DATE: 2001-11-15

FRIOR PELING DATE: 2001-11-15

FRIOR PELING DATE: 2001-11-29

FRIOR PELING DATE: 2001-11-29

FRIOR APPLICATION NUMBER: US 60/334,393

FRIOR PELING DATE: 2001-12-14

FRIOR PELING DATE: 2002-11-14

FRIOR PELING DATE: 2002-01-10

FRIOR PELING DATE: 2002-01-10

FRIOR PELING DATE: 2002-01-10

FRIOR PELING DATE: 2002-01-10

FRIOR APPLICATION NUMBER: US 60/347,319

FRIOR PELING DATE: 2002-01-10

FRIOR PELING DATE: 2002-02-08

FRIOR PELING DATE: 2002-02-08

FRIOR PELING DATE: 2002-02-08

FRIOR PELING DATE: 2002-02-08

FRIOR PELING DATE: 2002-02-03

FRIOR PELING DATE: 2002-02-13
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APPLICANT: Murray, Richard
APPLICANT: Mateon, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-01250003
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Publication No. US20030232350A1
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GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginaberg, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glynne, Richard
Hevezi, Peter A.
Mack, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 158; Conservative
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CORGANISM: Homo sapiens
US-10-295-027-781
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APPLICANT:
APPLICANT:
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                                                                                                                        APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Richard
APPLICANT: Murray, Richard
APPLICANT: Mack, David H.
APPLICANT: Wasenson, Susan R.
APPLICANT: Wasenson, Susan R.
APPLICANT: Eos Biotecchnology, Inc.
TITLE OF INVENTION: Methods of Disgnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: WHOMBER: US, 10,295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US, 60/350,666
PRIOR APPLICATION NUMBER: US, 60/350,666
PRIOR PILING DATE: 2001-11-13
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US, 60/340,376
PRIOR PELING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US, 60/340,376
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2002-01-00
PRIOR PELING DATE: 2002-01-10
PRIOR PELING DATE: 2003-01-10
PRIOR PELING DATE
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Publication No. US2003023250A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Watson, Susan R.
   Ginsberg, Wendy M
                                                                       Glynne, Richard
Hevezi, Peter A.
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ORGANISM: Homo sapiens
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US-10-295-027-781
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61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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PRIOR APPLICATION NUMBER: US 60/334,393

PRIOR FILING DATE: 2001-11-29

PRIOR PILING DATE: 2001-12-14

PRIOR PLING DATE: 2001-2-14

PRIOR PELING DATE: 2002-12-14

PRIOR PELING DATE: 2002-01-08

PRIOR PILING DATE: 2002-01-0

PRIOR PILING DATE: 2002-01-0

PRIOR PILING DATE: 2002-02-08

PRIOR PILING DATE: 2002-02-13

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1386
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Matches 158; Conservative
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                                                                                                   PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-15
PRIOR PELING DATE: 2001-11-12
PRIOR PELING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-12-14
PRIOR PELING DATE: 2002-12-14
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-01-08
PRIOR PELING DATE: 2002-01-09
PRIOR PELING DATE: 2002-01-09
PRIOR PELING DATE: 2002-01-09
PRIOR PELING DATE: 2002-01-09
PRIOR PELING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PELING DATE: 2002-02-13
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APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotecchnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer.
FILE REPRENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US 109/663,733
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PILING DATE: 2000-01-15
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
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                                              999'058/09
                                                                          LLING DATE: 2001-11-13
PPLICATION NUMBER: US 60/335,394
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Ginsberg, Wendy M.
Gish, Kurt C.
Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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Best Local Similarity 100.
Matches 158; Conservative
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CORGANISM: Homo sapiens
US-10-295-027-861
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